

SEQUENCE LISTING

GENERAL INFORMATION

(i) APPLICANT: Murphy, Patricia
White, Marga
Olson, Sheri
Yoshikawa, Matthew
Jackson, Geoffrey
Eskanderi, Tara
Schryer, Brenda

- (ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES OF THE HUMAN BRCA2 GENE
- (iii) NUMBER OF SEQUENCES: 110
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Howrey & Simon
 - (B) STREET: 1299 Pennsylvania Avenue N.W.

Park, Michael

- (C) CITY: Washington
- (D) STATE: DC
- (E) COUNTRY: USA
- (F) ZIP: 20004
- (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/084,471
 - (B) FILING DATE: 22 May 1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Halluin, Albert P
 - (B) REGISTRATION NUMBER: 25,227
 - (C) REFERENCE/DOCKET NUMBER: 53710031US02
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-463-8109
 - (B) TELEFAX: 650-463-8400
 - (C) TELEX:
 - (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE:	
(A) NAME/KEY: exon	
(B) LOCATION: 150	
(D) OTHER INFORMATION: Exon 5	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
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(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 182 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(11) MOLEGIE E ENDE Garante DIT	
(ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE:	
(IA) FRATORE.	
(A) NAME/KEY: exon	
(B) LOCATION: 1182	
(D) OTHER INFORMATION: Exon 15	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
ATTTAATTAC AAGTCTTCAG AATGCCAGAG ATATACAGGA TATGCGAATT AAGAAGAAAC	60
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CTCGAATCTC TCTGAAAGCA GCAGTAGGAG GCCAAGTTCC CTCTGCGTGT TCTCATAAAC	180
AG * ·	182
(a) THEODMARTON HOD GIO TO NO 2	
(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 188 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	

(ix) FEATURE:

(A) NAME/KEY: exon
(B) LOCATION: 1...188

(D) OTHER INFORMATION: Exon 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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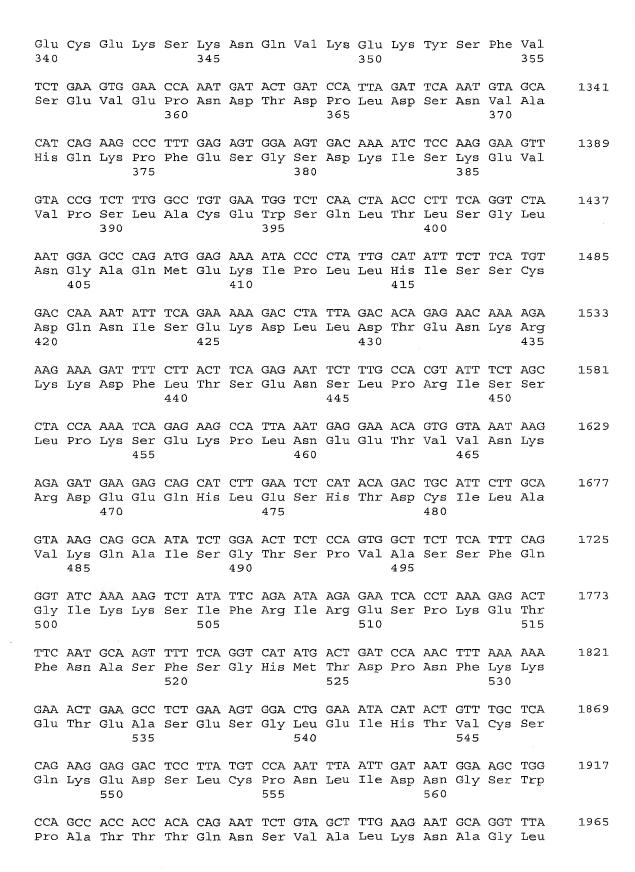
(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
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 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 229...10482
 - (D) OTHER INFORMATION: BRCA2 (OMI1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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			TTT AAG ACA CGC TGC Phe Lys Thr Arg Cys 15	285
			TGG TTT GAA GAA CTT Trp Phe Glu Glu Leu 35	333
- - - · · · · · · · · · · · · · · · · · ·			GCA GAA GAA TCT GAA Ala Glu Glu Ser Glu 50	381
			AAA ACT CCA CAA AGG Lys Thr Pro Gln Arg 65	429
			ATA ATA TTC AAA GAG Ile Ile Phe Lys Glu 80	477
			GTA AAA GAA TTA GAT Val Lys Glu Leu Asp 95	525
			AAT AGT AGA CAT AAA Asn Ser Arg His Lys 115	573

					AAA Lys											621
					TCT Ser											669
					CCA Pro											717
					AAG Lys											765
					GGA Gly 185											813
					CCA Pro											861
					TCT Ser											909
					TTT Phe											957
					TCT Ser											1005
					GGA Gly 265											1053
					GAC Asp											1101
					GAA Glu											1149
					TCT Ser											1197
					AGG Arg											1245
GAA	TGT	GAA	AAA	TCT	AAA	AAC	CAA	GTG	AAA	GAA	AAA	TAC	TCA	TTT	GTA	1293





565 570 575

	ACT Thr							2013
	ACA Thr							2061
	ATT Ile							2109
	ACA Thr 630							2157
	AGC Ser							2205
	TCT Ser							2253
	AAT Asn							2301
	AAT Asn							2349
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_	CAA Gln							2493
 	AGT Ser							2541
	ACT Thr							2589
 	GAA Glu 790							2637

GAA Glu	TCT Ser 805	GAT Asp	GTT Val	GAA Glu	TTA Leu	ACC Thr 810	AAA Lys	AAT Asn	ATT Ile	CCC Pro	ATG Met 815	GAA Glu	AAG Lys	AAT Asn	CAA Gln	2685
GAT Asp 820	GTA Val	TGT Cys	GCT Ala	TTA Leu	AAT Asn 825	GAA Glu	AAT Asn	TAT Tyr	AAA Lys	AAC Asn 830	GTT Val	GAG Glu	CTG Leu	TTG Leu	CCA Pro 835	2733
CCT Pro	GAA Glu	AAA Lys	TAC Tyr	ATG Met 840	AGA Arg	GTA Val	GCA Ala	TCA Ser	CCT Pro 845	TCA Ser	AGA Arg	AAG Lys	GTA Val	CAA Gln 850	TTC Phe	2781
AAC Asn	CAA Gln	AAC Asn	ACA Thr 855	AAT Asn	CTA Leu	AGA Arg	GTA Val	ATC Ile 860	CAA Gln	AAA Lys	AAT Asn	CAA Gln	GAA Glu 865	GAA Glu	ACT Thr	2829
ACT Thr	TCA Ser	ATT Ile 870	TCA Ser	AAA Lys	ATA Ile	ACT Thr	GTC Val 875	AAT Asn	CCA Pro	GAC Asp	TCT Ser	GAA Glu 880	GAA Glu	CTT Leu	TTC Phe	2877
TCA Ser	GAC Asp 885	AAT Asn	GAG Glu	AAT Asn	AAT Asn	TTT Phe 890	GTC Val	TTC Phe	CAA Gln	GTA Val	GCT Ala 895	AAT Asn	GAA Glu	AGG Arg	AAT Asn	2925
AAT Asn 900	CTT Leu	GCT Ala	TTA Leu	GGA Gly	AAT Asn 905	ACT Thr	AAG Lys	GAA Glu	CTT Leu	CAT His 910	Glu	ACA Thr	GAC Asp	TTG Leu	ACT Thr 915	2973
TGT Cys	GTA Val	AAC Asn	GAA Glu	CCC Pro 920	Ile	TTC Phe	AAG Lys	AAC Asn	TCT Ser 925	Thr	ATG Met	GTT Val	TTA Leu	TAT Tyr 930	GGA Gly	3021
GAC Asp	ACA Thr	GGT Gly	GAT Asp 935	Lys	CAA Gln	GCA Ala	ACC	CAA Gln 940	Val	TCA Ser	ATT	AAA Lys	AAA Lys 945	ASL	TTG Leu	3069
GTT Val	TAT Tyr	GTT Val 950	. Leu	GCA Ala	GAG Glu	GAG Glu	AAC Asr 955	і Гуя	AAT Asn	AGT Sei	GTA Val	A AAG Lys 960	GTI	G CAT	T ATA	3117
AAA Lys	ATG Met	Thr	CTA	GGT Gly	CAA Glr	GAT Asp 970	Let	A AAA	TCC S Ser	GA(2 ATC 5 Ile 975	s Sei	C TTO	3 AAT 1 Asr	T ATA	3165
GAT Asp 980	ь Гув	A ATA	A CCF	A GAA	A AAA 1 Lys 985	Asr	AA Ası	r GAT n Asp	TAC Tyi	C ATO	t Ası	C AAA	A TGO	G GCA o Ala	A GGA a Gly 995	3213
CTC Lev	TTA 1 Let	A GGT 1 Gly	r CC <i>I</i> y Pro	A ATT	e Sei	A AAT	CAC n His	C AG'	r TT r Pho	e Gl	A GG' y Gl	r AG y Se:	C TT r Ph	c AG e Ar 101	A ACA g Thr 0	3261
GCT Ala	TCA a Sei	A AA' r Ası	r AA0 n Ly: 101!	s Gl	A ATO	C AAG E Ly:	G CT	C TC' u Se: 102	r Gl	A CA u Hi	T AA s As	C AT	T AA e Ly 102	в гу	G AGC s Ser	3309

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	Cys					AAT Asn					Asp						3405
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	GTA Val	GTT Val	GTT Val	Ser	GAT Asp 1080	TGT Cys	AAA Lys	AAT Asn	Ser	CAT His 1085	ATA Ile	ACC Thr	CCT Pro	Gln	ATG Met 1090	TTA Leu	3501
	TTT Phe	TCC Ser	Lys	CAG Gln L095	GAT Asp	TTT Phe	AAT Asn	Ser	AAC Asn L100	CAT His	AAT Asn	TTA Leu	Thr	CCT Pro 1105	AGC Ser	CAA Gln	3549
	AAG Lys	Ala	GAA Glu 1110	ATT Ile	ACA Thr	GAA Glu	Leu	TCT Ser 1115	ACT Thr	ATA Ile	TTA Leu	Glu	GAA Glu 1120	TCA Ser	GGA Gly	AGT Ser	3597
	Gln					CAG Gln					Ser						3645
:	AGT Ser 1140	ACA Thr	TTT Phe	GAA Glu	Val	CCT Pro 1145	GAA Glu	AAC Asn	CAG Gln	Met	ACT Thr 1150	ATC Ile	TTA Leu	AAG Lys	Thr	ACT Thr 1155	3693
	TCT Ser	GAG Glu	GAA Glu	Cys	AGA Arg 1160	GAT Asp	GCT Ala	GAT Asp	Leu	CAT His 1165	GTC Val	ATA Ile	ATG Met	Asn	GCC Ala 1170	CCA Pro	3741
	TCG Ser	ATT Ile	Gly	CAG Gln 1175	GTA Val	GAC Asp	AGC Ser	Ser	AAG Lys 1180	CAA Gln	TTT Phe	GAA Glu	Gly	ACA Thr 1185	GTT Val	GAA Glu	3789
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	Ala	TCT Ser 1205	GGT Gly	TAT Tyr	TTA Leu	Thr	GAT Asp 1210	GAA Glu	AAT Asn	GAA Glu	Val	GGG Gly 1215	TTT Phe	AGG Arg	Gly	TTT Phe	3885
	TAT Tyr 1220	TCT Ser	GCT Ala	CAT His	Gly	ACA Thr 1225	AAA Lys	CTG Leu	AAT Asn	Val	TCT Ser 1230	ACT Thr	GAA Glu	GCT Ala	CTG Leu	CAA Gln 1235	3933
	TÀ2	GCT Ala	GTG Val	AAA Lys	. CTG Leu 1240	Phe	AGT Ser	GAT Asp	Ile	GAG Glu 1245	Asn	ATT Ile	AGT Ser	Glu	GAA Glu 1250	ACT Thr	3981
	TCT	GCA	GAG	GTA	CAT	' CCA	ATA	AGT	TTA	TCT	TCA	AGT	' AAA	TGT	CAI	GAT	4029

Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp 1255 1260 1265	
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val 1270 1275 1280	4077
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu 1285 1290 1295	4125
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg 1300 1305 1310 1315	4173
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320 1325 1330	4221
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335 1340 1345	4269
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350 1355 1360	4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375	4365
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380 1385 1390 1395	4413
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400 1405 1410	4461
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe 1415 1420 1425	4509
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe 1430 1435 1440	4557
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445 1450	4605
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460 1465 1470 1475	4653
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu	4701



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Phe		ACA Thr			Gly					Ile						4845
		GTG Val		Asn					Lys					Ser		4893
		AGT Ser	Phe					Ala					Tyr			4941
		AAA Lys					Ala					Glu				4989
	Pro	AAG Lys 1590				Met					Asn					5037
Leu		TCT Ser			Thr					Lys						5085
		AGA Arg		Thr					Thr					Phe		5133
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		TGT Cys					Ser					Ile				5229
	Leu	GCT Ala 1670				Ser					Thr					5277
Thr		TTA Leu			Ala					Arg						5325
	Gln	CCA Pro		Arg					Asp					Tyr		5373

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CTC TCC GAA Leu Ser Glu						Ser Asn	5469
AGC TAT TCC Ser Tyr Ser 1750	Tyr His	Ser Asp					5517
TCA AAA AAT Ser Lys Asn 1765				Glu Pro			5565
GAA GAT CAA Glu Asp Gln 1780	Lys Asn						5613
GAT GCA AAT Asp Ala Asn			Thr Val				5661
GAA CTT GTG Glu Leu Val						a Ala Ile	5709
AAA TTG TCC Lys Leu Ser		Asn Ser	Asn Asn		Val Gly Pro		5757
1830		1	.835		1840		
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TTT AGG ATA Phe Arg Ile	AAA GAC Lys Asp	GGT AAA Gly Lys 1850 ATA TTT	ATC GTT Ile Val	Cys Val 1 AGT TTC	TCA CAT GAZ Ser His Gli 855	Thr Ile	5805 5853
TTT AGG ATA Phe Arg Ile 1845 AAA AAA GTG Lys Lys Val	Ala Ser AAA GAC Lys Asp	GGT AAA Gly Lys 1850 ATA TTT Ile Phe 1865	ATC GTT Ile Val ACA GAC Thr Asp AAA ATT Lys Ile	Cys Val 1 AGT TTC Ser Phe 1870	TCA CAT GAZ Ser His Gli .855 AGT AAA GTZ Ser Lys Va.	A ATT AAG I le Lys 1875 I ATG GCA	
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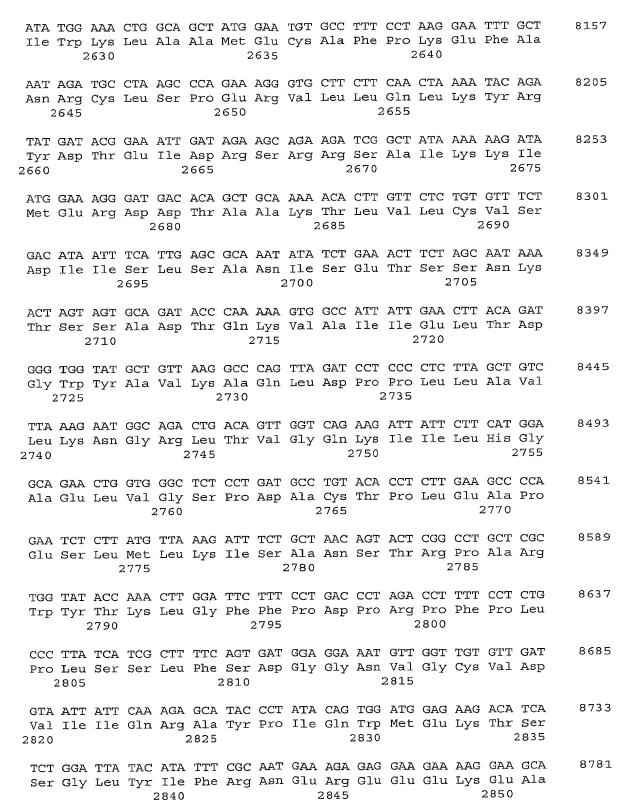
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		Thr	TGT Cys 1975				Ser					Lys				6189
	Ser		GCT Ala			Gln					Val		Ser			6237
Glu			ACC Thr		Gln					Val						6285
			GAC Asp	Gln					Glu					Arg		6333
			TTA Leu					Gly					Val			6381
		Ala	TTC Phe 2055				ser					Lys				6429
	Leu		AGT Ser			His					Val					6477
Asp			AGA Arg		Glu					Tyr						6525
			TCA Ser	Lys					Val					Pro		6573
			AAC Asn					Lys					Glu			6621
		Asn	AAC Asn 2135				Glu					Glu				6669
	Ile		GTT Val			Tyr					Gln					6717
CAG	TTG	GTA	ATT	GGA	ACC	AAA	GTC	TCA	CTT	GTT	GAG	AAC	ATT	CAT	GTT	6765

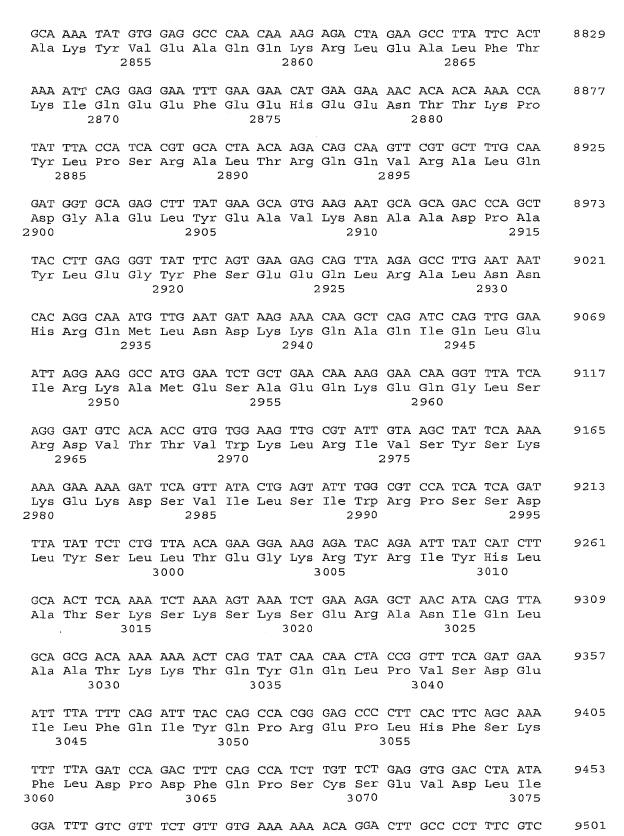
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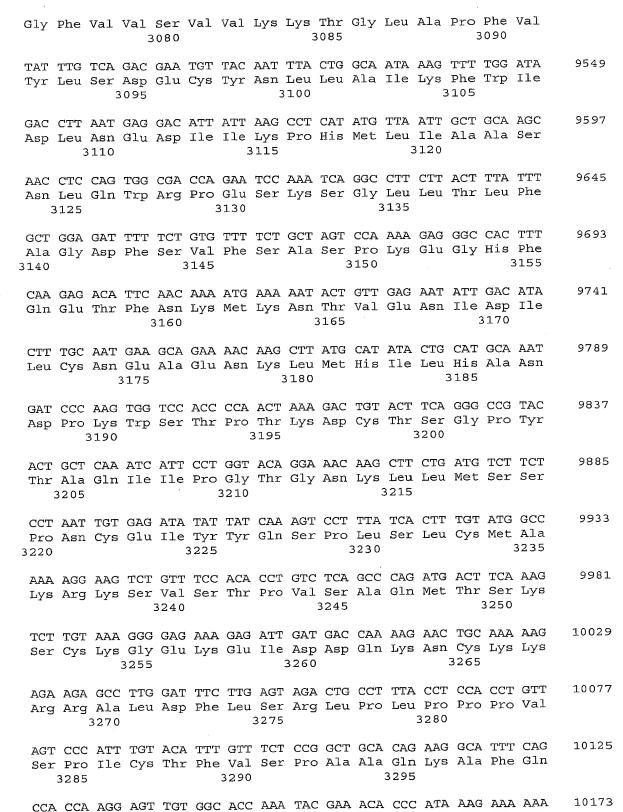
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2390 2395 2400

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				Arg	AAT Asn 2425				Glu					Lys	7533
			Gly		GGC Gly			Asp					Ile		7581
		Ile			TTT Phe		Lys					Gln			7629
	Thr				TGT Cys	Glu					Asp				7677
Leu					GAT Asp					Arg					7725
				Phe	CCA Pro 2505				Ser					Lys	7773
			Pro		ATC Ile			Lys					Gly		7821
		Ala			CAT His		Gln					Gly			7869
	Cys				AAC Asn	Ser					Ser				7917
Thr					GGT Gly					Trp					7965
				Gly	GGA Gly 2585				Pro					Lys	8013
			${\tt Glu}$		TAT Tyr			Leu					Gly	_	8061
		Leu			AGA Arg		Trp					Tyr			 8109









Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys

3315 3300 3305 3310 GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3340 3335 AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3355 3350 TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3375 3365 3370 CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3395 3385 3390 AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 10485 ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

 Met
 Pro
 Ile
 Gly
 Ser
 Lys
 Glu
 Arg
 Pro
 Thr
 Phe
 Phe
 Glu
 Ile
 Phe
 Lys
 Lys
 Lys
 Ala
 Asp
 Leu
 Gly
 Pro
 Ile
 Ser
 Leu
 Asp
 Phe
 Ile
 Phe
 Lys
 Ile
 Phe
 Ile
 Ile
 Phe
 Ile
 Ile
 Phe
 Lys
 Ile
 Ile</th

			100					105					110		
		115			Arg		120					125			
	130				Leu	135					140				
145					His 150					155					160
				165	His				170					175	
			180		Glu			185					190		
		195			Leu		200					205			
	210				Glu	215					220				
225					Lys 230					235					240
_	=			245	Phe				250					255	
			260		Ala			265					270		
		275			Ser		280					285			
	290				Glu	295					300				
305					Leu 310					315					320
				325	Ser				330					335	
			340		Glu			345					350		
		355			Val		360					365			
	370				Lys	375					380				
385					Ser 390					395					400
				405					410					415	
			420		. Asn			425					430		
		435			Asp		440					445			
	450				Lys	455					460				
465					Glu 470					475					480
				485					490					495	
			500		Lys			505					510		
_		515			Ala		520	l.				525			
	530	_			Glu	535					540				
Val 545		s Ser	. Glr	г гла	550		ser	ьеи	. cys	555		. шeu	тте	yan	560

Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu 1060 1065 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro 1085 1080 1075 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr 1100 1090 1095 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu 1110 1115 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile 1125 1130 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu 1150 1145 1140 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met 1155 1160 1165 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly 1170 1175 1180 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys 1190 1195 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe 1205 1210 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu 1225 1230 1220 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser 1235 1240 1245 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys 1250 1255 1260 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp 1275 1270 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn 1285 1290 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn 1310 1305 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser 1320 1325 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn 1335 1340 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp 1350 1355 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly 1365 1370 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val

1015

1030

1045

1380

1460

1445

1395

Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr

Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln

1020

1035

1050

1450

1420

1435

1385

Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln 1400

Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser

Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys

Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu

Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys 1465

1415

1430

Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met

Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arq Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg 2100 2105 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys 2115 2120 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu 2130 2135 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met 2185 2190 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln



Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly 2390 2395 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys 2435 2440 2445 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Pro Leu Asp Leu 2470 2475 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly 2515 2520 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu

2840 2845 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala 2855 2860 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr 2870 2875 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg 2885 2890 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala 2905 2900 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala 2920 2925 2915 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile 2935 2940 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln 2955 2945 2950 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser 2975 2965 2970 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro 2980 2985 2990 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile 2995 3000 3005 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn 3015 3020 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val 3030 3035 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His 3045 3050 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val 3060 3065 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala 3075 3080 3085 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys 3100 3090 3095 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile 3105 3110 3115 312 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu 3130 3125 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu 3145 3150 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn 3155 3160 3165 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu 3180 3175 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser 3190 3195 320 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu 3210 3205 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu 3220 3225 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met 3245 3240 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn 3260 3255 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro 3270 3275 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys 3290 3285



Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile 3300 3305 3310 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe 3320 3315 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu 3340 3335 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys 3355 3350 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser 3370 3365 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys 3385 3380 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys 3405 3400 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile 3415

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 229...10482
 - (D) OTHER INFORMATION: BRCA2 (OMI2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTGGCGCGA G TCTGCTGCGC C ACAGATTTGT G CTGGAGCGGA C	TCGGGTGTC TT ACCGGCGCG GT	TTTGCGGCG GTC	GGTCGCC TTACTCCG	GCCGGGAGAA G GCCAAAAAAG A AGGTAAAA ATG	CGTGAGGGG ACTGCACCT	60 120 180 237
GGA TCC AAA Gly Ser Lys 5	GAG AGG CCA Glu Arg Pro	ACA TTT TTT Thr Phe Phe 10	GAA ATT Glu Ile	TTT AAG ACA Phe Lys Thr 15	CGC TGC Arg Cys	285
AAC AAA GCA Asn Lys Ala 20	GAT TTA GGA Asp Leu Gly 25	CCA ATA AGT Pro Ile Ser	CTT AAT Leu Asn 30	TGG TTT GAA Trp Phe Glu	GAA CTT Glu Leu 35	333
TCT TCA GAA Ser Ser Glu						381
CAT AAA AAC His Lys Asn						429



AAA Lys	CCA Pro	TCT Ser 70	TAT Tyr	AAT Asn	CAG Gln	CTG Leu	GCT Ala 75	TCA Ser	ACT Thr	CCA Pro	ATA Ile	ATA Ile 80	TTC Phe	AAA Lys	GAG Glu	477
CAA Gln	GGG Gly 85	CTG Leu	ACT Thr	CTG Leu	CCG Pro	CTG Leu 90	TAC Tyr	CAA Gln	TCT Ser	CCT Pro	GTA Val 95	AAA Lys	GAA Glu	TTA Leu	GAT Asp	525
AAA Lys 100	TTC Phe	AAA Lys	TTA Leu	GAC Asp	TTA Leu 105	GGA Gly	AGG Arg	TAA Asn	GTT Val	CCC Pro 110	AAT Asn	AGT Ser	AGA Arg	CAT His	AAA Lys 115	573
				GTG Val 120												621
TGT Cys	CCA Pro	CTT Leu	CTA Leu 135	AAT Asn	TCT Ser	TGT Cys	CTT Leu	AGT Ser 140	GAA Glu	AGT Ser	CCT Pro	GTT Val	GTT Val 145	CTA Leu	CAA Gln	669
TGT Cys	ACA Thr	CAT His 150	GTA Val	ACA Thr	CCA Pro	CAA Gln	AGA Arg 155	GAT Asp	AAG Lys	TCA Ser	GTG Val	GTA Val 160	TGT Cys	GGG Gly	AGT Ser	717
TTG Leu	TTT Phe 165	CAT His	ACA Thr	CCA Pro	AAG Lys	TTT Phe 170	GTG Val	AAG Lys	GGT Gly	CGT Arg	CAG Gln 175	ACA Thr	CCA Pro	AAA Lys	CAT His	765
ATT Ile 180	TCT Ser	GAA Glu	AGT Ser	CTA Leu	GGA Gly 185	GCT Ala	GAG Glu	GTG Val	GAT Asp	CCT Pro 190	GAT Asp	ATG Met	TCT Ser	TGG Trp	TCA Ser 195	813
AGT Ser	TCT Ser	TTA Leu	GCT Ala	ACA Thr 200	CCA Pro	CCC Pro	ACC Thr	CTT Leu	AGT Ser 205	TCT Ser	ACT Thr	GTG Val	CTC Leu	ATA Ile 210	GTC Val	861
AGA Arg	AAT Asn	GAA Glu	GAA Glu 215	GCA Ala	TCT Ser	GAA Glu	ACT Thr	GTA Val 220	TTT Phe	CCT Pro	CAT His	GAT Asp	ACT Thr 225	ACT Thr	GCT Ala	909
AAT Asn	GTG Val	AAA Lys 230	AGC Ser	TAT Tyr	TTT Phe	TCC Ser	AAT Asn 235	His	GAT Asp	GAA Glu	AGT Ser	CTG Leu 240	AAG Lys	AAA Lys	AAT Asn	957
GAT Asp	AGA Arg 245	Phe	ATC Ile	GCT Ala	TCT Ser	GTG Val 250	ACA Thr	GAC Asp	AGT Ser	GAA Glu	AAC Asn 255	ACA Thr	AAT Asn	CAA Gln	AGA Arg	1005
GAA Glu 260	Ala	GCA Ala	AGT Ser	CAT His	GGA Gly 265	Phe	GGA Gly	AAA Lys	ACA Thr	TCA Ser 270	Gly	AAT Asn	TCA Ser	TTT Phe	AAA Lys 275	1053
GTA Val	AAT Asn	AGC Ser	TGC Cys	AAA Lys 280	Asp	CAC His	ATT Ile	GGA Gly	AAG Lys 285	Ser	ATG Met	CCA Pro	AAT Asn	GTC Val 290	CTA Leu	1101
GAA	. GAT	GAA	GTA	TAT	' GAA	ACA	GTT	' GTA	GAT	ACC	TCT	' GAA	GAA	GAT	AGT	1149

Glu	Asp	Glu	Val 295	Tyr	Glu	Thr	Val	Val 300	Asp	Thr	Ser	Glu	Glu 305	Asp	Ser	
						AAA Lys										1197
						AAA Lys 330										1245
						AAC Asn										1293
						GAT Asp										1341
						AGT Ser										1389
						GAA Glu										1437
						AAA Lys 410										1485
						AAA Lys										1533
						TCA Ser										1581
					_	CCA Pro										1629
						CTT Leu										1677
						GGA Gly 490										1725
						TTC Phe										1773
						GGT Gly										1821

520 525 530

									-
	ACT Thr								1869
	AAG Lys								1917
	GCC Ala 565								1965
	TCC Ser								2013
	GAA Glu								2061
	CTA Leu								2109
	CTT Leu								2157
	AGA Arg 645								2205
	AGC Ser								2253
	TCT Ser								2301
	TGT Cys								2349
	CTG Leu								2397
	AAA Lys 725								2445
	GTA Val								2493

	AA AGT ys Sei								2541
	CT ACT								2589
	AA GAA ys Glu 790	Ser							2637
Glu S	CT GAT er Ası 05								2685
	TA TGT al Cys								2733
	AA AAA lu Lys								2781
	AA AAC In Asr								2829
	CA ATT er Ile 870	Ser							2877
Ser A	AC AAT sp Asr 85								2925
	TT GCT eu Ala								2973
_	TA AA(al Asr	-							3021
	CA GGT								3069
	'AT GTT 'yr Va] 950	Leu							3117
Lys M	TG ACT let Thi								3165

	AA ATA vs Ile														3213
	TA GGT eu Gly	Pro					Ser					Phe			3261
	CA AAT er Asn					Leu					Ile				3309
	TG TTC et Phe 1030				Ile					Pro					3357
	T GAA al Glu 15			Asn					Asp						3405
	AG CCT 's Pro	_	Ser	_			_	Ser	_			_	Ser		3453
GTA GT Val Va	T GTT	Ser					Ser					Gln			3501
	CC AAG er Lys					Ser					Thr				3549
	CA GAA a Glu 1110				Leu					Glu					3597
	TT GAA ne Glu 25			Gln					Ser						3645
	CA TTT nr Phe		Val					Met					Thr		3693
	AG GAA .u Glu	Cys					Leu					Asn			3741
	T GGT e Gly					Ser					Gly				3789
	AA CGG /s Arg 1190				Gly					Asp					3837
GCT TO	CT GGT	TAT	TTA	ACA	GAT	GAA	AAT	GAA	GTG	GGG	TTT	AGG	GGC	TTT	3885

Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly 1205 1210 1215	Phe
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu 1220 1225 1230 1	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu 1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys Cys His 1255 1260 1265	
TCT GTC GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr 1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile 1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys 1300 1305 1310 1	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn 1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr 1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His 1350	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr 1365	
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys 1380 1385 1390 1	
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr 1400 1405 1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr 1415 1420 1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser	

1430 1435 1440

Asn					Phe					Pro	GAA Glu L455					4605
TTT Phe 1460	TCC Ser	TTA Leu	AAT Asn	Ser	GAA Glu L465	TTA Leu	CAT His	TCT Ser	Asp	ATA Ile 470	AGA Arg	AAG Lys	AAC Asn	ГЛЗ	ATG Met L475	4653
GAC Asp	ATT Ile	CTA Leu	Ser	TAT Tyr L480	GAG Glu	GAA Glu	ACA Thr	Asp	ATA Ile 1485	GTT Val	AAA Lys	CAC His	Lys	ATA Ile L490	CTG Leu	4701
AAA Lys	GAA Glu	Ser	GTC Val 1495	CCA Pro	GTT Val	GGT Gly	Thr	GGA Gly 500	AAT Asn	CAA Gln	CTA Leu	Val	ACC Thr 1505	TTC Phe	CAG Gln	4749
GGA Gly	Gln	CCC Pro 1510	GAA Glu	CGT Arg	GAT Asp	Glu	AAG Lys L515	ATC Ile	AAA Lys	GAA Glu	CCT Pro	ACT Thr 1520	CTG Leu	TTG Leu	GGT Gly	4797
Phe	CAT His 1525	ACA Thr	GCT Ala	AGC Ser	Gly	AAA Lys 1530	AAA Lys	GTT Val	AAA Lys	Ile	GCA Ala 1535	AAG Lys	GAA Glu	TCT Ser	TTG Leu	4845
GAC Asp 1540	TA PYY	GTG Val	AAA Lys	Asn	CTT Leu 1545	TTT Phe	GAT Asp	GAA Glu	Lys	GAG Glu 1550	CAA Gln	GGT Gly	ACT Thr	Ser	GAA Glu 1555	4893
ATC Ile	ACC Thr	AGT Ser	Phe	AGC Ser 1560	CAT His	CAA Gln	TGG Trp	Ala	AAG Lys 1565	ACC Thr	CTA Leu	AAG Lys	Tyr	AGA Arg 1570	GAG Glu	4941
GCC Ala	TGT Cys	Lys	GAC Asp 1575	CTT Leu	GAA Glu	TTA Leu	Ala	TGT Cys 1580	GAG Glu	ACC Thr	ATT Ile	Glu	ATC Ile 1585	ACA Thr	GCT Ala	4989
GCC Ala	Pro	AAG Lys 1590	Cys	AAA Lys	GAA Glu	Met	CAG Gln 1595	AAT Asn	TCT Ser	CTC Leu	Asn	AAT Asn 1600	GAT Asp	AAA Lys	AAC Asn	5037
Leu	GTT Val 1605	Ser	ATT	GAG Glu	Thr	GTG Val 1610	GTG Val	CCA Pro	CCT Pro	Lys	CTC Leu 1615	TTA Leu	AGT Ser	GAT Asp	AAT Asn	5085
TTA Leu 1620	Cys	AGA Arg	CAA Gln	Thr	GAA Glu 1625	Asn	CTC Leu	AAA Lys	Thr	TCA Ser 1630	Lys	AGT Ser	ATC Ile	TTT Phe	TTG Leu 1635	5133
AAA Lys	. GTT Val	' AAA Lys	Val	CAT His	Glu	AAT Asn	GTA Val	GAA Glu	AAA Lys 1645	Glu	ACA Thr	GCA Ala	AAA Lys	AGT Ser 1650	CCT Pro	5181
GCA Ala	ACT Thr	TGT Cys	TAC Tyr	Thr	AAT Asn	CAG Gln	Ser	CCT Pro 1660	Tyr	TCA Ser	GTC Val	ATT	GAA Glu	Asn	'TCA Ser	5229

GCC TTA GCT Ala Leu Ala 1670	Phe Tyr Thr	AGT TGT AGT Ser Cys Ser 1675	AGA AAA ACT Arg Lys Thr	TCT GTG AGT Ser Val Ser 680	CAG 5277 Gln
ACT TCA TTA Thr Ser Leu 1685	. Leu Glu Ala	AAA AAA TGG Lys Lys Trp 1690	CTT AGA GAA Leu Arg Glu 1695	GGA ATA TTT Gly Ile Phe	GAT 5325 Asp
			GAT TAT GTA Asp Tyr Val 1710	Gly Asn Tyr	
		Ser Thr Ile	GCT GAA AAT Ala Glu Asn 1725		
			AGT AAC AGT Ser Asn Ser		
AGC TAT TCC Ser Tyr Ser 1750	Tyr His Ser	GAT GAG GTA Asp Glu Val 1755	TAT AAT GAT Tyr Asn Asp	TCA GGA TAT Ser Gly Tyr .760	CTC 5517 Leu
			GAG CCA GTA Glu Pro Val 1775		
		Ser Phe Ser	AAA GTA ATA Lys Val Ile 1790	Ser Asn Val	
			AAT GAA GAT Asn Glu Asp 1805		
			AAA AAT AAA Lys Asn Lys		
AAA TTG TCC Lys Leu Se 1830	r Ile Ser Asn	AGT AAT AAT Ser Asn Asn 1835	TTT GAG GTA Phe Glu Val	GGG CCA CCT Gly Pro Pro 1840	GCA 5757 Ala
TTT AGG ATA Phe Arg Ile 1845	A GCC AGT GGT e Ala Ser Gly	AAA ATC GTT Lys Ile Val 1850	TGT GTT TCA Cys Val Ser 1855	CAT GAA ACA His Glu Thr	ATT 5805 Ile
AAA AAA GTO Lys Lys Vai 1860	G AAA GAC ATA l Lys Asp Ile 1865	Phe Thr Asp	AGT TTC AGT Ser Phe Ser 1870	Lys Val Ile	AAG 5853 Lys 1875
GAA AAC AA Glu Asn As	C GAG AAT AAA n Glu Asn Lys 1880	A TCA AAA ATT S Ser Lys Ile	TGC CAA ACG Cys Gln Thr 1885	AAA ATT ATG Lys Ile Met 1890	GCA 5901 Ala

	lu Ala Leu Asp		GAT ATT CTT CAT Asp Ile Leu His 1905	Asn Ser	5949
	sp Glu Cys Ser		A CAT AAG GTT TTT His Lys Val Phe 1920		5997
			C CAA AAT ATG TCT n Gln Asn Met Ser 1935		6045
			GGTT AGT TTG GAA Val Ser Leu Glu 1950		6093
			CAT AAG TCA GTC His Lys Ser Val		6141
	ys Gly Ile Phe		A AGT GGA AAA TCT a Ser Gly Lys Ser 1985	Val Gln	6189
			A CAA GTG TTT TCT g Gln Val Phe Ser 2000		6237
		Phe Ser Lys	A GTA TTG TTT AAF S Val Leu Phe Lys 2015		6285
			A AAT ACT GCT ATA 1 Asn Thr Ala Ile 2030		6333
			r TCA TAT AAT GTO e Ser Tyr Asn Val		6381
	he Ser Gly Phe		A AGT GGA AAG CAA a Ser Gly Lys Glr 2069	n Val Ser	6429
			G GGA GTG TTA GAG S Gly Val Leu Glu 2080		6477
		Ser Leu Hi	C TAT TCA CCT ACC s Tyr Ser Pro Thi 2095		6525
			I GAT AAG AGA AAd l Asp Lys Arg Asi 2110		6573
CAC TGT GTA A	AC TCA GAA ATG	GAA AAA AC	C TGC AGT AAA GA	AAA TTT A	6621

His	Cys	Val		Ser 2120	Glu	Met	Glu	_	Thr 2125	Cys	Ser	Lys		Phe 2130	Lys	
		AAT Asn					Glu					Glu				6669
	Ile	AAA Lys 2150				Tyr					Gln					6717
Gln		GTA Val			Thr					Val						6765
		AAA Lys		Gln					Asn					Ile		6813
		GAA Glu	Thr					Pro	_				Ile			6861
		ACT Thr					Ser					Glu				6909
	Glu	ATT Ile 2230				Phe					Glu					6957
Lys		CCA Pro			Ala					Phe						7005
		ATG Met		Leu					Ile					Gly		7053
		ATC Ile	Leu					Ser					Leu			7101
		GAC Asp					Asn					Leu				7149
	Ser	ACT Thr 2310				Thr					Arg					7197
His		TCT Ser			Pro					Pro						7245
		CAA Gln														7293

2350 2355 2340 TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT 7341 Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2365 2360 TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2380 2375 ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC 7437 Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT 7485 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2410 2415 2405 GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA 7533 Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2430 2435 2420 2425 AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581 Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp 7629 AAT GAG ATT CAT CAG TTT AAC AAA AAC TCC AAT CAA GCA GCA GCT Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala 2460 2455 GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser 2470 2475 CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725 Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Gln 2490 2485 AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773 Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr 2515 2500 TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT 7821 Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val 2520 CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA 7869 Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys 2540 2535 CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC 7917 His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His 2555 2550 ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile 2570 2565

				Gly					Pro		AAT Asn			Lys		8013
			Glu					Leu			ACT Thr		Gly			8061
		Leu					Trp				CAC His	Tyr				8109
	Trp					Met					CCT Pro 2					8157
Asn					Pro					Leu	CAA Gln 2655					8205
				Ile					Arg		GCT Ala			Lys		8253
			Asp					Lys			GTT Val		Cys			8301
		Ile					Asn				ACT Thr	Ser				8349
	Ser					${\tt Gln}$					ATT Ile					8397
Gly					Lys					Pro	CCC Pro 2735					8445
TTA Leu 2740	AAG Lys	AAT Asn	GGC Gly	Arg	CTG Leu 2745	ACA Thr	GTT Val	GGT Gly	Gln	AAG Lys 2750	ATT Ile	ATT Ile	CTT Leu	His	GGA Gly 2755	8493
			Val					Ala			CCT Pro		Glu			8541
		Leu					Ser				ACT Thr	Arg				8589
TGG Trp	Tyr	ACC Thr 2790	AAA Lys	CTT Leu	GGA Gly	Phe	TTT Phe 2795	CCT Pro	GAC Asp	CCT Pro	AGA Arg	CCT Pro 2800	TTT Phe	CCT Pro	CTG Leu	8637

Pro	TTA Leu 2805				Phe					Asn						8685
	ATT			Arg					Gln					Thr		8733
	GGA Gly		Tyr					Glu					ГХг			8781
	AAA Lys	Tyr					Gln					Ala				8829
	ATT Ile					Glu					Asn					8877
Tyr	TTA Leu 2885				Ala					Gln						8925
	GGT Gly			Leu					Lys					Pro		8973
	CTT Leu		Gly					Glu					Leu			9021
	AGG Arg	Gln					Lys					Ile				9069
	AGG Arg					Ser					Glu					9117
Arg	GAT Asp 2965				Val					Ile						9165
	GAA Glu			Ser					Ile					Ser		9213
	TAT		Leu					Lys					Tyr			9261
	ACT Thr	Ser					Lys					Asn				9309
GCA	GCG	ACA	AAA	AAA	ACT	CAG	TAT	CAA	CAA	CTA	CCG	GTT	TCA	GAT	GAA	9357

Ala Ala Thr 3030	Lys Lys Thr	Gln Tyr Gln 3035	Gln Leu Pro	Val Ser Asp 040	Glu
ATT TTA TTT	Gln Ile Tyr	CAG CCA CGG	GAG CCC CTT Glu Pro Leu 3055	CAC TTC AGC	
			TGT TCT GAG Cys Ser Glu 3070	Val Asp Leu	
		Val Lys Lys	ACA GGA CTT : Thr Gly Leu :		
Tyr Leu Ser			CTG GCA ATA . Leu Ala Ile		
			CAT ATG TTA . His Met Leu 3		
	Trp Arg Pro		TCA GGC CTT Ser Gly Leu: 3135		
			AGT CCA AAA Ser Pro Lys 3150	Glu Gly His	
		Met Lys Asn	ACT GTT GAG . Thr Val Glu . 3165		
Leu Cys Asn			ATG CAT ATA Met His Ile		,
			GAC TGT ACT Asp Cys Thr 3		
	Ile Ile Pro		AAC AAG CTT Asn Lys Leu 3215		
			CCT TTA TCA Pro Leu Ser 3230	Leu Cys Met	
		Thr Pro Val	TCA GCC CAG Ser Ala Gln : 3245		
			GAC CAA AAG Asp Gln Lys		

3255

3260

3265

AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT 10077 Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val 3275 3280 AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG 10125 Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln 3290 3295 3285 CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA 10173 Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys 3300 3305 3310 3315 GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3340 3335 AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3350 3355 TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375 CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Glu Glu 3380 3385 3390 3395 AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 10485 ATT ACA ACT AAA AAA TAT ATC TAA

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid

Ile Thr Thr Lys Lys Tyr Ile 3415

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Pro Ile Gly Ser Lys Glu Arq Pro Thr Phe Phe Glu Ile Phe Lys

10 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe 25 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu 40 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr 55 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 75 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 90 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser 105 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 120 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 150 155 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr 170 165 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met 180 185 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val 200 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp 215 220 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu 230 235 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr 245 250 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn 265 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro 280 Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu 295 300 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu 310 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr 345 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser 360 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser 375 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu 390 395 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile 405 410 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu 425 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg 440 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val 455

Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr

Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val

Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys 1250 1255 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly

Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Phe Glu Val Gly

Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg

Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn

Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu 2500 2505 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile

2745 2750 2740 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu 2765 2760 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg 2775 2780 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro 2790 2795 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly 2810 2805 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu 2830 2825 2820 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu 2840 2845 2835 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala 2855 2860 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr 2870 2875 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg 2885 2890 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala 2900 2905 2910 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala 2915 2920 2925 Leu Asn Asn His Arq Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile 2935 2940 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln 2950 2955 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser 2965 2970 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro 2980 2985 2990 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile 2995 3000 3005 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn 3015 3020 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val 3030 3035 304 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His 3045 3050 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val 3060 3065 3070 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala 3075 3080 3085 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys 3095 3100 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile 3110 3115 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu 3130 3125 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu 3145 3140 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn 3160 3165 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu 3175 3180 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser 3195 3190

Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu 3210 3205 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu 3225 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met 3240 3245 3235 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn 3260 3255 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro 3275 3270 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys 3290 3285 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile 3310 3300 3305 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe 3320 3325 3315 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu 3340 3335 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys 3350 3355 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser 3365 3370 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys 3385 3380 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys 3400 3395 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile 3410 3415

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 229...10482
 - (D) OTHER INFORMATION: BRCA2 (OMI3)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCGA GCTTCTGAAA	CTAGGCGGCA	GAGGCGGAGC	CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC	TTTTGCGGCG	GTGGGTCGCC	GCCGGGAGAA GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG	GTTTTTGTCA	GCTTACTCCG	GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTTACC	AAGCATTGGA	GGAATATCGT	AGGTAAAA ATG CCT ATT	237
			Met Pro Ile	
			1	

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
5 10 15

					GGA Gly 25								_			333
					CCC Pro											381
					TAC Tyr											429
					CAG Gln											477
					CCG Pro											525
					TTA Leu 105											573
					AAA Lys											621
					TCT Ser											669
					CCA Pro											717
					AAG Lys											765
					GGA Gly 185											813
					CCA Pro											861
					TCT Ser											909
					TTT Phe											957
GAT	AGA	TTT	ATC	GCT	TCT	GTG	ACA	GAC	AGT	GAA	AAC	ACA	AAT	CAA	AGA	1005



Asp	Arg 245	Phe	Ile	Ala	Ser	Val 250	Thr	Asp	Ser	Glu	Asn 255	Thr	Asn	Gln	Arg	
		GCA Ala														1053
		AGC Ser														1101
		GAA Glu														1149
		TTA Leu 310														1197
		AGC Ser														1245
		GAA Glu														1293
		GTG Val														1341
		AAG Lys														1389
		TCT Ser 390														14,37
		GCC Ala														1485
		AAT Asn														1533
		GAT Asp														1581
		AAA Lys														1629
AGA Arg	GAT Asp	GAA Glu	GAG Glu	CAG Gln	CAT His	CTT Leu	GAA Glu	TCT Ser	CAT His	ACA Thr	GAC Asp	TGC Cys	ATT Ile	CTT Leu	GCA Ala	1677

470 475 480

AAG Lys 485								1725
ATC Ile								1773
AAT Asn								1821
ACT Thr		_						1869
AAG Lys								1917
GCC Ala 565								1965
TCC Ser								2013
GAA Glu								2061
CTA Leu								2109
CTT Leu								2157
AGA Arg 645								2205
AGC Ser								2253
TCT Ser								2301
TGT Cys								2349

	CTG Leu															2397
	AAA Lys 725															2445
	GTA Val															2493
	AAA Lys															2541
	CCT Pro															2589
	AAA Lys															2637
	TCT Ser 805															2685
	GTA Val															2733
	GAA Glu															2781
	CAA Gln															2829
	TCA Ser															2877
	GAC Asp 885															2925
AAT Asn 900	CTT Leu	GCT Ala	TTA Leu	GGA Gly	AAT Asn 905	ACT Thr	AAG Lys	GAA Glu	CTT Leu	CAT His 910	GAA Glu	ACA Thr	GAC Asp	TTG Leu	ACT Thr 915	2973
															GGA Gly	3021



												AAA Lys				3069
												AAG Lys 960				3117
												TCC Ser				3165
												AAA Lys				3213
			Pro					Ser				AGC Ser	Phe			3261
		Asn					Leu					ATT Ile				3309
	Met					Ile					Pro	ACT Thr 1040				3357
Cys					Asn					Asp		CAA Gln				3405
				Ser					Ser			TTA Leu		Ser		3453
			Ser					Ser				CCT Pro	Gln			3501
		Lys					Ser					ACA Thr				3549
	Ala					Leu					Glu	GAA Glu 1120				3597
${\tt Gln}$					Gln					Ser		ATA Ile				3645
				Val					Met			TTA Leu		Thr		3693
TCT	GAG	GAA	TGC	AGA	GAT	GCT	GAT	CTT	CAT	GTC	ATA	ATG	AAT	GCC	CCA	3741

Ser	Glu	Glu	_	Arg 1160	Asp	Ala	Asp		His 1165	Val	Ile	Met		Ala 1170	Pro	
		Gly					Ser					Gly		GTT Val		3789
	Lys					Gly					Asp			AAA Lys		3837
Ala					Thr					Val				GGC Gly		3885
				Gly					۷al					CTG Leu		3933
			Lys					Ile					Glu	GAA Glu 1250		3981
		Glu					Ser					Lys		CAT His		4029
	Val					Lys					Asn			ACT Thr		4077
7 ~ ·							~~~	ama			~~~					
Ser					ГЛа					Leu				ATT Ile		4125
Ser ATG	Glu 1285 ACT	Lys	Asn GGC	Asn ACT Thr	Lys	Cys L290 GTT	Gln GAA	Leu GAA	Ile ATT Ile	Leu ACT	Gln 1295 GAA	Asn AAT	Asn	Ile AAG Lys	Glu AGA	4125 4173
ATG Met 1300	Glu 1285 ACT Thr	Lys ACT Thr	GGC Gly AAT Asn	Asn ACT Thr	Lys TTT Phe 1305 GAT	Cys L290 GTT Val	Gln GAA Glu AAA	GAA Glu TAT Tyr	ATT Ile	Leu ACT Thr 1310 GCT	Gln 1295 GAA Glu GCC	Asn AAT Asn	TAC Tyr AGA Arg	Ile AAG Lys	Glu AGA Arg 1315	
ATG Met 1300 AAT Asn	Glu 1285 ACT Thr ACT Thr	ACT Thr GAA Glu TTA Leu	GGC Gly AAT Asn GAA	Asn ACT Thr GAA Glu 1320 TTT	TTT Phe 1305 GAT Asp	Cys L290 GTT Val AAC Asn	Gln GAA Glu AAA Lys AGT Ser	GAA Glu TAT Tyr	ATT Ile ACT Thr 1325 TCA	ACT Thr 1310 GCT Ala	Gln 1295 GAA Glu GCC Ala	AAT AGT Ser AAT ASn	Asn TAC Tyr AGA Arg	AAG Lys AAT Asn	AGA Arg 1315 TCT Ser	4173
ATG Met 1300 AAT Asn CAT His	Glu 1285 ACT Thr ACT Thr AAC ASD	ACT Thr GAA Glu TTA Leu	GGC Gly AAT Asn GAA Glu 1335	ASN ACT Thr GAA Glu 1320 TTT Phe	TTT Phe 1305 GAT Asp GAT Asp	Cys 1290 GTT Val AAC Asn GGC Gly	GAA Glu AAA Lys AGT Ser	GAA Glu TAT Tyr GAT Asp 1340	ATT Ile ACT Thr 1325 TCA Ser	ACT Thr 1310 GCT Ala AGT Ser	Gln 1295 GAA Glu GCC Ala AAA Lys	AST AST SET AAT AST	TAC Tyr AGA Arg GAT Asp 1345	AAG Lys AAT Asn 1330	AGA Arg 1315 TCT Ser GTT Val	4173 4221
ATG Met 1300 AAT Asn CAT His TGT Cys	Glu 1285 ACT Thr ACT Thr AAC Asn ATT Ile	ACT Thr GAA Glu TTA Leu CAT His 1350 CTT	GGC Gly AAT Asn GAA Glu 1335 AAA Lys	ASN ACT Thr GAA Glu 1320 TTT Phe GAT ASP	TTT Phe 1305 GAT Asp GAT Asp GAA Glu TCT Ser	Cys 1290 GTT Val AAC Asn GGC Gly ACG Thr	GAA Glu AAA Lys AGT Ser GAC Asp	GAA Glu TAT Tyr GAT Asp 1340 TTG Leu	ATT Ile ACT Thr 1325 TCA Ser CTA Leu	ACT Thr 1310 GCT Ala AGT Ser TTT Phe	Gln 1295 GAA Glu GCC Ala AAA Lys ACT Thr	AST AST SET AAT ASD ASP 1360	Asn TAC Tyr AGA Arg GAT Asp 1345 CAG Gln AAC	AAG Lys AAT Asn 1330 ACT Thr	AGA Arg 1315 TCT Ser GTT Val AAC Asn	4173 4221 4269

CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn



				Thr	GAA Glu 1625				Thr					Phe		5133
			Val		GAA Glu			Glu					Lys			5181
		Cys			AAT Asn		Ser					Ile				5229
	Leu				ACA Thr	Ser					Thr					5277
Thr					GCA Ala					Arg						5325
				Arg	ATA Ile 1705				Asp					Tyr		5373
			Asn		AAC Asn			Ile					Lys			5421
		Glu			GAT Asp		Tyr					Ser				5469
Ser	Tyr 1	Ser 1750	Tyr	His	TCT Ser	Asp	Glu 1755	Val	Tyr	Asn	Asp	Ser L760	Gly	Tyr	Leu	5517
Ser					GAT Asp					Pro						5565
				Asn	ACT Thr 1785				Lys					Val		5613
			Ala		CCA Pro			Val					Cys			5661
		Val			TCT Ser		Pro					Asn				5709
	Leu				AAT Asn	Ser					Val					5757



	Phe					Gly					Val	TCA Ser 1855					5805
					Asp					Ser		AGT Ser			Ile		5853
				Glu					Ile			ACG Thr		Ile			5901
			Tyr					Asp				ATT Ile	Leu				5949
		Asp					Ser					AAG Lys					5997
	Ile					Ile					Gln	AAT Asn 1935					6045
]					Lys					Asp		AGT Ser			Thr		6093
				Lys					Lys			AAG Lys		Val			6141
			Thr					Ser				GGA Gly	Lys				6189
		Ser					Gln					GTG Val					6237
	Glu					Gln					Val	TTG Leu 2015					6285
					Gln					Glu		ACT Thr			Arg		6333
				Leu					Gly			TAT Tyr		Val			6381
			Ala					Ser				GGA Gly	Lys				6429
	ATT	TTA	GAA	AGT	TCC	TTA	CAC	AAA	GTT	AAG	GGA	GTG	TTA	GAG	GAA	TTT	6477

Ile Le	u Glu 2070	Ser	Ser	Leu		Lys 2075	Val	Lys	Gly		Leu 2080	Glu	Glu	Phe	
GAT TT Asp Le 208	u Ile			Glu					Tyr						6525
CAA AA Gln As 2100			Lys					Val					Pro		6573
CAC TG His Cy		Asn					Lys					Glu			6621
TTA TC Leu Se	r Asn					Glu					Glu				6669
TCT AT Ser Il					Tyr					Gln					6717
CAG TT Gln Le 216	u Val			Thr					Val						6765
TTG GG Leu Gl 2180			Gln					Asn					Ile		6813
AAA AC Lys Th		Thr					Pro					Ile			6861
TGT TC Cys Se		TAC	TCC	7\7\7\	O.7. m										
		Tyr 215				Ser					Glu				6909
GTA GA Val Gl	2 A ATT	215 GCT	Ser AAA	Lys GCT	Asp TTT Phe	Ser 2 ATG	Glu 220 GAA	Asn GAT	Tyr GAT	Phe GAA Glu	Glu 2 CTG	Thr 2225 ACA	Glu GAT	Ala TCT	6909 6957
	A ATT u Ile 2230 G CCA u Pro	GCT Ala	Ser AAA Lys CAT	GCT Ala GCC Ala	Asp TTT Phe 2	Ser 2 ATG Met 235 CAT	Glu 220 GAA Glu TCT	Asn GAT Asp CTT	Tyr GAT Asp TTT Phe	Phe GAA Glu 2 ACA	Glu 2 CTG Leu 240 TGT	Thr 225 ACA Thr	Glu GAT Asp GAA	Ala TCT Ser	
Val Gl	A ATT u Ile 2230 G CCA u Pro 5	GCT Ala AGT Ser	AAA Lys CAT His TTG Leu	Lys GCT Ala GCC Ala 2 TCA	TTT Phe 2 ACA Thr 250 AAT	Ser 2 ATG Met 235 CAT His	Glu 2220 GAA Glu TCT Ser	Asn GAT Asp CTT Leu ATT	Tyr GAT Asp TTT Phe 2	GAA Glu 2 ACA Thr 2255	CTG Leu 240 TGT Cys	Thr 2225 ACA Thr CCC Pro	GAT Asp GAA Glu GGA Gly	TCT Ser AAT Asn	6957
AAA CT- Lys Le 224 GAG GA Glu GI	A ATT u Ile 2230 G CCA u Pro 5 A ATG u Met	GCT Ala AGT Ser GTT Val	AAA Lys CAT His TTG Leu 2	GCT Ala GCC Ala TCA Ser 265	TTT Phe 2 ACA Thr 250 AAT Asn	ATG Met 235 CAT His TCA Ser	Glu 220 GAA Glu TCT Ser AGA Arg	Asn GAT Asp CTT Leu ATT Ile 2	GGA GGA GGA GLY 270	GAA Glu 2 ACA Thr 2255 AAA Lys	CTG Leu 240 TGT Cys AGA Arg	Thr 2225 ACA Thr CCC Pro AGA Arg	GAT Asp GAA Glu GGA Gly	TCT Ser AAT Asn GAG Glu 2275	6957 7005

		2	295				2	300				2	305			
	Ser					Thr					Arg			ATG Met		7197
His					Pro					Pro				ACT Thr		7245
GAA Glu 2340	CGT Arg	CAA Gln	GAG Glu	Ile	CAG Gln 2345	AAT Asn	CCA Pro	AAT Asn	Phe	ACC Thr 350	GCA Ala	CCT Pro	GGT Gly	CAA Gln	GAA Glu 2355	7293
			Lys					Glu					Glu	AAA Lys 2370		7341
TCA Ser	AGC Ser	Asn	TTA Leu 2375	GCA Ala	GTT Val	TCA Ser	Gly	CAT His 2380	CCA Pro	TTT Phe	TAT Tyr	Gln	GTT Val 2385	TCT Ser	GCT Ala	7389
ACA Thr	Arg	AAT Asn 2390	GAA Glu	AAA Lys	ATG Met	Arg	CAC His 2395	TTG Leu	ATT Ile	ACT Thr	Thr	GGC Gly 2400	AGA Arg	CCA Pro	ACC Thr	7437
Lys					Pro					Ser				AGA Arg		7485
GAA Glu 2420	CAG Gln	TGT Cys	GTT Val	Arg	AAT Asn 2425	ATT Ile	AAC Asn	TTG Leu	Glu	GAA Glu 2430	AAC Asn	AGA Arg	CAA Gln	AAG Lys	CAA Gln 2435	7533
			Gly					Asp					Ile	AAT Asn 2450		7581
		Ile					Lys					Gln		GCA Ala		7629
	Thr					Glu					Asp			ACA Thr		7677
Leu	CAG Gln 2485	AAT Asn	GCC Ala	AGA Arg	Asp	ATA Ile 2490	CAG Gln	GAT Asp	ATG Met	Arg	ATT Ile 2495	AAG Lys	AAG Lys	AAA Lys	CAA Gln	7725
	Gln			Phe					Ser					AAA Lys		7773
TCC Ser	ACT Thr	CTG Leu	Pro	CGA Arg 2520	ATC Ile	TCT Ser	CTG Leu	Lys	GCA Ala 2525	GCA Ala	GTA Val	GGA Gly	GGC Gly	CAA Gln 2530	GTT Val	7821



	GCG TGT Ala Cys 2535		Lys Gln					7869
His Cys	ATA AAA Ile Lys 2550				Glu Ser			7917
	GAT TAT	Phe Gly						7965
	GCT GAT Ala Asp			Ile Pro				8013
	GAA GAA Glu Glu					Pro Gly		8061
	CTT ATT Leu Ile 2615		Ile Trp					8109
Ile Trp	AAA CTG Lys Leu 2630				Phe Pro			8157
	TGC CTA Cys Leu	Ser Pro						8205
	ACG GAA Thr Glu			Arg Arg				8253
	AGG GAT Arg Asp					Leu Cys		8301
	ATT TCA Ile Ser 2695		Ala Asn					8349
Thr Ser	AGT GCA Ser Ala 2710				Ile Ile			8397
Thr Ser	Ser Ala 2710 TAT GCT Tyr Ala	Asp Thr GTT AAG Val Lys	Gln Lys 2715 GCC CAG	Val Ala	Ile Ile	Glu Leu 2720 CTC TTA	Thr Asp	8397 8445

			Val					Ala					Glu	GCC Ala 2770		8541
		Leu					Ser					Arg		GCT Ala		8589
	Tyr					Phe					Arg			CCT Pro		8637
Pro					Phe					Asn				GTT Val		8685
				Arg					Gln					ACA Thr		8733
			Tyr					Glu					Lys	GAA Glu 2850		8781
		Tyr					Gln					Ala		TTC Phe		8829
	Ile					Glu					Asn			AAA Lys		8877
Tyr					Ala		Thr			Gln				TTG Leu		8925
				Leu					Lys					CCA Pro		8973
			Gly					Glu					Leu	AAT Asn 2930		9021
		Gln					Lys					Ile		TTG Leu		9069
	Arg					Ser					Glu			TTA Leu		9117
Arg			-		Val					Ile				TCA Ser		9165
AAA	GAA	AAA	GAT	TCA	GTT	ATA	CTG	AGT	ATT	TGG	CGT	CCA	TCA	TCA	GAT	9213



Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp 2980 2990 2985 TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT 9261 Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3005 3000 GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA 9309 Ala Thr Ser Lys Ser Lys Ser Glu Arq Ala Asn Ile Gln Leu 3015 3020 GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA 9357 Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030 3035 ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA 9405 Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3050 TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA 9453 Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3065 3070 GGA TTT GTC GTT TCT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501 Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3085 TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA 9549 Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3100 GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC 9597 Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3115 AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT 9645 Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3130 GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT 9693 Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3145 3150 CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA 9741 Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT 9789 Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC 9837 Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3195 ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT 9885 Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser

3205 3210 3215

				Ile					Pro		TCA Ser			Met	9933
			Ser					Val			CAG Gln		Thr		9981
		Lys					Ile				AAG Lys	Asn			10029
-	Arg					Leu					TTA Leu				10077
Ser					Phe					Ala	CAG Gln 3295				10125
				Cys					Glu		CCC Pro			Lys	10173
			Ser					Pro			AAA Lys		Asn		10221
		Leu					Ile				GAA Glu	Leu			10269
	Thr					Ser					GAA Glu				10317
Ser					Thr					Thr	AGT Ser 3375				10365
				Arg					Ser	-	ATC Ile			Gln	10413
			Ala					Cys			AAT Asn		Gln		10461
	ACA Thr	Thr				ATC Ile	TAA								10485

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu 40 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 85 90 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser 100 105 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 120 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 150 155 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr 170 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met 185 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val 200 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp 215 220 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu 235 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr 245 250 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn 265 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro 280 His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu 295 300 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu 310 315 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala 325 330 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr 340 345 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser 360



Asn Val Ala Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu

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Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp

Lys Thr Val' Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp

a 1

Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser

Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys 2050 2055 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu 2130 2135 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn

Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met

Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Pro Leu Asp Leu Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys

Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu

2710 2725 2740 2745 2755 2760 2775 2790 2805 2820 2825 2835 2840 2850 2855

2645

2665 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu 2680 2685 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser 2695 2700 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu 2715 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu 2730 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile 2750 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu 2765 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg 2780 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro 2795 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly 2810 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu 2845 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala 2860 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr 2865 2870 2875 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg 2885 2890 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala 2900 2905 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala 2920 2925 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile 2935 2940 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln 2950 2955 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser 2965 2970 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro 2985 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile 3000 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn 3015 3020 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val 3030 3035 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His 3050 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val 3065 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala 3080 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys 3095

2650

Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile

Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu 3125 3130 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu 3145 3140 3150 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn 3160 3165 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu 3175 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser 3190 3195 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu 3205 3210 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu 3225 3220 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met 3235 3240 3245 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn 3255 3260 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro 3270 3275 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys 3285 3290 3295 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile 3305 3310 3300 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe 3315 3320 3325 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu 3335 3340 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys 3350 3355 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser 3370 Glu Asp Tyr Leu Arg Leu Lys Arg Cys Thr Thr Ser Leu Ile Lys 3385

Glu Glu Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys 3395 3400 3405

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3115

3110

(2) INFORMATION FOR SEQ ID NO:10:

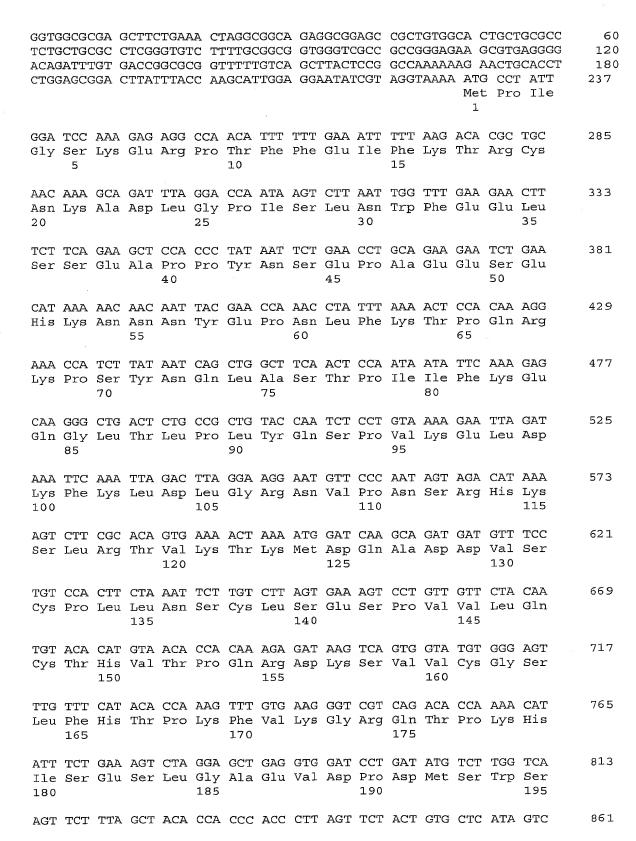
3415

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10485 base pairs
 - (B) TYPE: nucleic acid

Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 229...10482
 - (D) OTHER INFORMATION: BRCA2 (OMI4)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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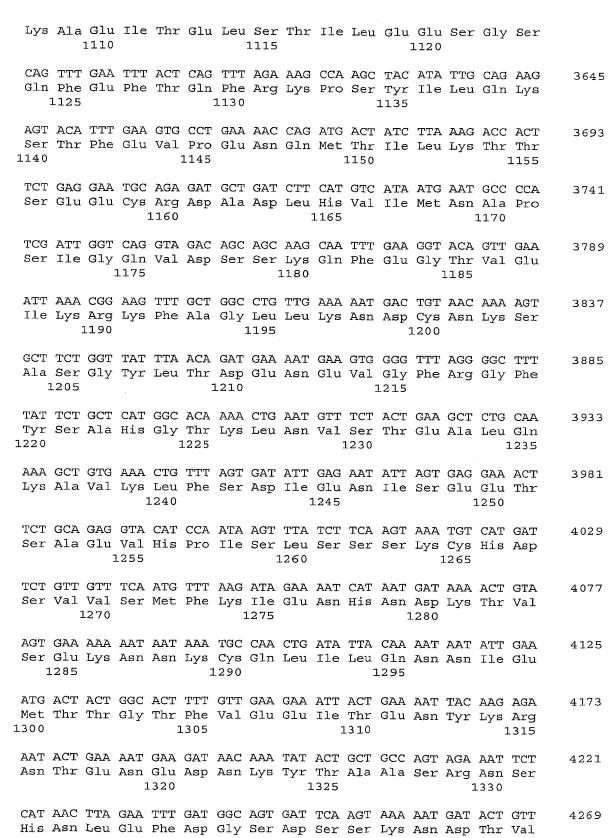


Ser	Ser	Leu	Ala	Thr 200	Pro	Pro	Thr	Leu	Ser 205	Ser	Thr	Val	Leu	Ile 210	Val	
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					TTT Phe											957
					TCT Ser											1005
					GGA Gly 265											1053
					GAC Asp											1101
					GAA Glu											1149
					TCT Ser											1197
	_			_	AGG Arg			_	_			_		_		1245
					AAA Lys 345											1293
			Glu		AAT Asn			Asp		Leu						1341
					GAG Glu											1389
					TGT Cys											1437
					GAG Glu											1485
					GAA Glu											1533

420	425	430	435
		TCT TTG CCA CGT ATT Ser Leu Pro Arg Ile :	
		GAG GAA ACA GTG GTA 2 Glu Glu Thr Val Val 4 465	
		CAT ACA GAC TGC ATT (His Thr Asp Cys Ile 1480	
		CCA GTG GCT TCT TCA 1 Pro Val Ala Ser Ser 1 495	
		AGA GAA TCA CCT AAA (Arg Glu Ser Pro Lys (510	
		ACT GAT CCA AAC TTT A Thr Asp Pro Asn Phe 1 525	
		GAA ATA CAT ACT GTT Glu Ile His Thr Val 6	
		TTA ATT GAT AAT GGA ALLEU Ile Asp Asn Gly 6	
		GCT TTG AAG AAT GCA (AAA AAA AAA AAA AAA AAA AAA AAA AAA	
		AAG TTT ATT TAT GCT A Lys Phe Ile Tyr Ala 3 590	
		ATA CCG AAA GAC CAA I Ile Pro Lys Asp Gln 1 605	
		GAA GCA AAT GCT TTT (Glu Ala Asn Ala Phe (625	
		GGT TTA TTG CAT TCT : Gly Leu Leu His Ser : 640	
		GAA GAA CCA ACT TTG Glu Glu Pro Thr Leu 655	

ACT Thr 660	Ser	TCT Ser	TTT Phe	GGG Gly	ACA Thr 665	ATT Ile	CTG Leu	AGG Arg	AAA Lys	TGT Cys 670	TCT Ser	AGA Arg	AAT Asn	GAA Glu	ACA Thr 675	2253
											GAT Asp					2301
											ACC Thr					2349
TCT Ser	CTG Leu	TCA Ser 710	TGC Cys	CTG Leu	CAG Gln	GAA Glu	GGA Gly 715	CAG Gln	TGT Cys	GAA Glu	AAT Asn	GAT Asp 720	CCA Pro	AAA Lys	AGC Ser	2397
											GCT Ala 735					2445
											ACT Thr					2493
											AGC Ser					2541
											GTC Val					2589
											AAA Lys					2637
											ATG Met 815					2685
GAT Asp 820	GTA Val	TGT Cys	GCT Ala	TTA Leu	AAT Asn 825	GAA Glu	AAT Asn	TAT Tyr	AAA Lys	AAC Asn 830	GTT Val	GAG Glu	CTG Leu	TTG Leu	CCA Pro 835	2733
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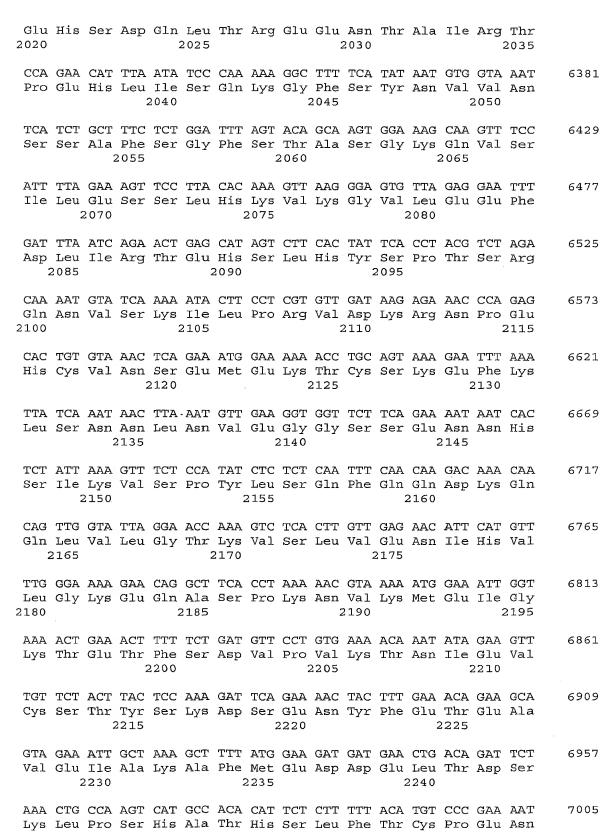
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		GCT Ala														2973
		AAC Asn														3021
		GGT Gly														3069
		GTT Val 950														3117
		ACT Thr														3165
		ATA Ile														3213
		GGT Gly	Pro					Ser					Phe			3261
		AAT Asn					Leu					Ile				3309
	Met	TTC Phe				Ile					Pro					3357
CAa		GAA Glu			Asn					Asp						3405
		CCT Pro		Ser					Ser					Ser		3453
		GTT Val	Ser					Ser					Gln			3501
		AAG Lys 1					Ser					Thr				3549
AAG	GCA	GAA	ATT	ACA	GAA	CTT	TCT	ACT	ATA	TTA	GAA	GAA	TCA	GGA	AGT	3597



		1	.335				-	1340				:	1345		
TGT A Cys I	le E	_				Thr					Thr				4317
ATA T Ile C 13					Ser					Lys					4365
ATT A Ile L 1380				Leu					Phe					Lys	4413
CAA G Gln G			Cys					Ser					Leu		4461
ACT A Thr L		Chr					Lys					Ser			4509
TTT C Phe G	ln 7					Lys					Ala				4557
AAT A Asn L 14	ys]				Phe					Pro					4605
TTT T Phe S 1460				Ser					Asp					Lys	4653
GAC A Asp I			Ser					Asp					Lys		4701
AAA G Lys G		Ser					Thr					Val			4749
GGA C Gly G	ln F					Glu					Pro				4797
TTT C. Phe H 15	is T				Gly					Ile					4845
GAC A Asp L 1540				Asn					Lys					Ser	4893
ATC A			Phe					Ala					Tyr		4941

Ala Cys Lys	GAC CTT GAA TTA Asp Leu Glu Leu 1575			Thr Ala
	TGT AAA GAA ATG Cys Lys Glu Met			
	ATT GAG ACT GTG Ile Glu Thr Val 1610			
	CAA ACT GAA AAT Gln Thr Glu Asn 1625	Leu Lys Thr		
	GTA CAT GAA AAT Val His Glu Asn 1640			
Ala Thr Cys	TAC ACA AAT CAG Tyr Thr Asn Gln 1655			
	TTT TAC ACA AGT Phe Tyr Thr Ser			
	CTT GAA GCA AAA Leu Glu Ala Lys 1690			
	GAA AGA ATA AAT Glu Arg Ile Asn 1705	Thr Ala Asp		
	AAT TCA AAC AGT Asn Ser Asn Ser 1720			
Leu Ser Glu	AAA CAA GAT ACT Lys Gln Asp Thr 1735			Ser Asn
	TAC CAT TCT GAT Tyr His Ser Asp			
	AAA CTT GAT TCT Lys Leu Asp Ser 1770			
	AAA AAC ACT AGT		GTA ATA TCC AAT	

GAT Asp	'GCA Ala	AAT Asn	Ala	TAC Tyr 1800	CCA Pro	CAA Gln	ACT Thr	Val	AAT Asn 1805	GAA Glu	GAT Asp	ATT Ile	Cys	GTT Val 1810	GAG Glu	5661
		GTG Val					Pro					Asn				5709
	Leu	TCC Ser 1830				Ser					Val					5757
Phe	AGG Arg 1845	ATA Ile	GCC Ala	AGT Ser	Gly	AAA Lys 1850	ATC Ile	GTT Val	TGT Cys	Val	TCA Ser 1855	CAT His	GAA Glu	ACA Thr	ATT Ile	5805
AAA Lys 1860	AAA Lys	GTG Val	AAA Lys	Asp	ATA Ile 1865	TTT Phe	ACA Thr	GAC Asp	Ser	TTC Phe 1870	AGT Ser	AAA Lys	GTA Val	Ile	AAG Lys 1875	5853
		AAC Asn	Glu					Ile					Ile			5901
		TAC Tyr 1					Asp					Leu				5949
	Asp	AAT Asn 1910				Ser					Lys					5997
Ile		AGT Ser			Ile					Gln						6045
		GTT Val		Lys					Asp					Thr		6093
		TGT Cys	Lys					Lys					Val			6141
GCA Ala	AAT Asn	ACT Thr 1	TGT Cys 975	GGG Gly	ATT Ile	TTT Phe	Ser	ACA Thr .980	GCA Ala	AGT Ser	GGA Gly	Lys	TCT Ser 985	GTC Val	CAG Gln	6189
	Ser	GAT Asp .990				Gln					Val					6237
Glu	GAT Asp 2005	AGT Ser	ACC Thr	AAG Lys	Gln	GTC Val 010	TTT Phe	TCC Ser	AAA Lys	Val	TTG Leu 015	TTT Phe	AAA Lys	AGT Ser	AAC Asn	6285
GAA	CAT	TCA	GAC	CAG	CTC .	ACA	AGA	GAA	GAA	AAT	ACT	GCT	ATA	CGT	ACT	6333



2245		2250		2255	
	Met Val Leu		Arg Ile G	GA AAA AGA A ly Lys Arg A 70	7053
				AA AGA AAC T ys Arg Asn I	7101
		Ile Glu Asn		AA TCC TTA A ys Ser Leu I 23	7149
Lys Ser T				GA AGA TTG T arg Arg Leu I 2320	7197
				CCC TTT CGC A Pro Phe Arg T 2335	7245
	Sln Glu Ile		Asn Phe T	ACC GCA CCT C Thr Ala Pro C .50	7293
				TG ACT TTG G eu Thr Leu G	7341
		Val Ser Gly		TTT TAT CAA G Phe Tyr Gln V 23	7389
Thr Arg A				ACT ACA GGC A Thr Thr Gly A 2400	7437
				CCG CAT TTT C Ser His Phe F 2415	7485
	Cys Val Arg		Leu Glu G	AAA AAC AGA C lu Asn Arg C 30	7533
				AA AAT AAG A ys Asn Lys I	7581
		Phe Asn Lys		CC AAT CAA G Ser Asn Gln A 24	7629

GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677

Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser

2475

CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Gln 2485 2490 2495	7725
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr 2500 2505 2510	7773
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val 2520 2525 2530	·7821
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys 2535 2540 2545	7869
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His 2550 2560	7917
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile 2565 2570 2575	7965
CAG TTG GCT GAT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala 2580 2585	8013
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp 2600 2605	8061
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile 2615 2620 2625	8109
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala 2630 2635 2640	8157
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg 2645 2650 2655	8205
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile 2660 2665 2670 2675	8253
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser 2680 2685 2690	8301
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys 2695 2700 2705	8349

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp 2710 2715 2720	8397
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val 2725 2730 2735	8445
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly 2740 2745 2750 2755	8493
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770	8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785	8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800	8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp 2805 2810 2815	8685
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser 2820 2825 2830 2835	8733
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala 2840 2845 2850	8781
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr 2855 2860 2865	8829
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro 2870 2875 2880	8877
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln 2885 2890 2895	8925
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala 2900 2905 2910 2915	8973
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn 2920 2925 2930	9021
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069

His	Arg		Met 2935	Leu	Asn	Asp	-	Lys 2940	Gln	Ala	Gln		Gln 2945	Leu	Glu	
	Arg					Ser		GAA Glu			Glu					9117
Arg					Val			TTG Leu		Ile						9165
				Ser				AGT Ser	Ile					Ser		9213
			Leu					AAG Lys					Tyr			9261
		Ser					Lys	TCT Ser 3020				Asn				9309
	Ala					Gln		CAA Gln			Pro					9357
Ile					Tyr			CGG Arg		Pro						9405
				Asp				TCT Ser	Cys					Leu		9453
			Va1					TAR TAR					Pro			9501
		Ser	Asp	Glu	Cys	Tyr	Asn	TTA Leu 3100	Leu	Ala		Lys	Phe	${\tt Trp}$		9549
	Leu					Ile		CCT Pro			Leu					9597
Asn					Pro			AAA Lys		Gly						9645
				Ser				GCT Ala	Ser					His		9693
								AAT Asn								9741

3160 3165 3170

			-	3100				~	703				-	31/0		
		Asn	Glu				Lys	Leu				Leu	His			9789
	Pro	Lys				Pro	Thr				Thr	Ser				9837
Thr	Ala				Pro	Gly				Lys	Leu					9885
Pro				Ile	Tyr				Pro	Leu				Met	Ala	9933
			Ser	Val				Val	Ser				Thr	Ser		9981
		Lys	Gly				Ile	Asp				Asn	Cys			10029
	Arg	Ala				Leu	Ser				Leu	Pro				10077
Ser	Pro				Phe	Val				Ala	${\tt Gln}$					10125
Pro				Cys	Gly				Glu	Thr				Lys	Lys	10173
			Ser	Pro				Pro	Phe				Asn	Glu		10221
		Leu	Glu				Ile	Ala				Leu	Ala			10269
	\mathtt{Thr}	${\tt Gln}$				Ser	${\tt Gl}_{Y}$				Glu	Lys				10317
Ser	Val				Thr	Arg				Thr	Ser					10365
Leu				Arg	Arg				Ser	Leu				Gln	Glu	10413
	GAT Asp ACT Thr CCT Pro 220 AAA Lys TCT Ser AGA Arg AGT Ser CCA Pro 300 GAA Glu TCT Ser AAT Asn TCT Ser	Leu Cys GAT CCC Asp Pro ACT GCT Thr Ala 3205 CCT AAT Pro Asn 220 AAA AGG Lys AGA Arg AGA Arg Arg AGT CCC Ser Pro 3285 CCA CCA Pro Pro 300 GAA CTG Glu Leu TCT CTT Ser Leu AAT ACC Asn Thr TCT GTC Ser Val 3365 CTC AGA Leu Arg	Leu Cys Asn GAT CCC AAG Asp Pro Lys 3190 ACT GCT CAA Thr Ala Gln 3205 CCT AAT TGT Pro Asn Cys 220 AAA AGG AAG Lys Arg Lys AGA AGA GCC ATT Ser Pro Ile 3285 CCA CCA AGG Pro Pro Arg 300 GAA CTG AAT Glu Leu Asn TCT CTT TTG Ser Leu Leu AAT ACC CAA Asn Thr Gln 3350 TCT GTC AGT Ser Val Ser 3365 CTC AGA CTG Leu Arg Leu	CTT TGC AAT GAA Leu Cys Asn Glu 3175 GAT CCC AAG TGG Asp Pro Lys Trp 3190 ACT GCT CAA ATC Thr Ala Gln Ile 3205 CCT AAT TGT GAG Pro Asn Cys Glu 220 AAAA AGG AAG TCT Lys Arg Lys Ser 3255 AGA AGA GCC TTG ATG AAA GGG ATG CCC ATT TGT Ser Pro Ile Cys 3285 CCA CCA AGG AGT Pro Pro Arg Ser 300 GAA CTG AAT TCT Glu Leu Asn Ser 3335 AAT ACC CAA GCT Asn Thr Gln Ala Ser Val Ser Glu S3365 CTC AGA CTG AAA Leu Arg Leu Lys	CTT TGC AAT GAA GCA Leu Cys Asn Glu Ala 3175 GAT CCC AAG TGG TCC Asp Pro Lys Trp Ser 3190 ACT GCT CAA ATC ATT Thr Ala Gln Ile Ile 3205 CCT AAT TGT GAG ATA Pro Asn Cys Glu Ile 220 AAA AGG AAG TCT GTT Lys Arg Lys Ser Val 3240 TCT TGT AAA GGG GAG Ser Cys Lys Gly Glu 3255 AGA AGA GCC TTG GAT Arg Ala Leu Asp 3270 AGT CCC ATT TGT ACA Ser Pro Ile Cys Thr 3285 CCA CCA AGG AGT TGT Pro Pro Arg Ser Cys 3300 GAA CTG AAT TCT CCT Glu Leu Asn Ser Pro 3320 TCT CTT TTG GAA AGT Ser Leu Leu Glu Ser 3335 AAT ACC CAA GCT CTT Asn Thr Gln Ala Leu 3350 CTC GTC AGA CTG AAA CGA Leu Arg Leu Lys Arg	CTT TGC AAT GAA GCA GAA Leu Cys Asn Glu Ala Glu 3175 GAT CCC AAG TGG TCC ACC Asp Pro Lys Trp Ser Thr 3190 ACT GCT CAA ATC ATT CCT Thr Ala Gln Ile Ile Pro 3205 CCT AAT TGT GAG ATA TAT Pro Asn Cys Glu Ile Tyr 220 AAA AGG AAG TCT GTT TCC Lys Arg Lys Gly Glu Lys 3240 TCT TGT AAA GGG GAG AAA Ser Cys Lys Gly Glu Lys 3255 AGA AGA GCC TTG GAT TCC Arg Arg Ala Leu Asp Phe 3285 CCA CCA AGG AGT TGT GGC Pro Pro Arg Ser Cys Gly 300 GAA CTG AAT TCT CCT CAG Glu Leu Asn Ser Pro Gln 3320 TCT CTT TTG GAA AGT AAT Ser Leu Leu Glu Ser Asn 3335 AAT ACC CAA GCT CTT TTG Asn Thr Gln Ala Leu Leu 3356 CTC AGA CTG AGT GAA CGT CTT Ser Val Ser Glu Ser Thr 3365 CTC AGA CTG AAT CAT Ser Thr 3365	CTT TGC AAT GAA GCA GAA AAC Leu Cys Asn Glu Ala Glu Asn 3175 GAT CCC AAG TGG TCC ACC CCA Asp Pro Lys Trp Ser Thr Pro Gly 3205 ACT GCT CAA ATC ATT CCT GGT Thr Ala Gln Ile Ile Pro Gly 3210 CCT AAT TGT GAG ATA TAT TAT TAT Pro Asn Cys Glu Ile Tyr Tyr 3225 AAA AGG AAG TCT GTT TCC ACA Lys Arg Lys Gly Glu Lys Glu Ser Thr 3240 TCT TGT AAA GGG GAG AAA GAG Ser Cys Lys Gly Glu Lys Glu Ser Thr 3240 AGA AGA GCC TTG GAT TTC TTG AAA GAG Ser Pro Ile Cys Thr Phe Val 3225 CCA CCA ATT TGT ACA TTT GTT Ser Pro Arg Ser Cys Gly Thr 3300 GAA CTG AAT TCT CCT CAG ATG Glu Leu Asn Ser Pro Gln Met 3320 TCT CTT TTG GAA AGT ATT TCT CTT CAG ATG Glu Leu Asn Ser Pro Gln Met 33305 TCT CTT TTG GAA AGT TCT TTG TCT AAT TCA ASn TCT GTT AAT TCA ASn Trr GIn Aa AGT AAT TCA ASn Trr GIn Aa AGT AAT TCA ASn Trr GIn Aaa AGT AAT TCA AGG ATG AAT AAT TCA AGT AAT TCA AGT AAT TCA AGT AAT AGT AAT ACG AAT AAT TCA AAT TCA AGT AAT TCA AGT AAT ACG AAT AAT ACC AAT AAT ACG AAT AAT ACG AAT AAT ACC AAT AAT ACC AAT AAT ACC AAT AAT	CTT TGC AAT GAA GCA GAA AAC AAG Leu Cys Asn Glu Ala Glu Asn Lys 3175 GAT CCC AAG TGG TCC ACC CCA ACT Asp Pro Lys Trp Ser Thr Pro Thr 3190 ACT GCT CAA ATC ATT CCT GGT ACA CTT Ala Glu Ile Pro Gly Thr 3210 CCT AAT TGT GAG ATA TAT TAT CAA Pro Asn Cys Glu Ile Tyr Tyr Gln 2220 AAA AGG AAG TCT GTT TCC ACA CCT Lys Arg Lys Ser Val Ser Thr Pro 3240 TCT TGT AAA GGG GAG AAA GAG ATT Ser Cys Lys Gly Glu Lys Glu Ile Ser Arg Arg Ala Leu Asp Phe Leu Ser 3270 AGG CCC ATT TGT ACA TTC TGT ACA TTC TGT AGT ASP Arg Arg Ser Cys Thr Phe Val Ser 3285 CCA CCA AGG AGT TGT GGT TCT TCT TCT GTT ACT AAA AGG AGT TTC TTC TCT GET ACA TTT TCT AGT ACA ACT ACT	CTT TGC AAT GAA GCA GAA AAC AAG CTT Leu Cys Asn Glu Ala Glu Asn Lys Leu 3175 GAT CCC AAG TGG TCC ACC CCA ACT AAA Asp Pro Lys Trp Ser Thr Pro Thr Lys 3190 ACT GCT CAA ATC ATT CCT GGT ACA GGA Thr Ala Gln Ile Ile Pro Gly Thr Gly 3210 CCT AAT TGT GAG ATA TAT TAT CAA AGT Pro Asn Cys Glu Ile Tyr Tyr Gln Ser 220 AAA AGG AAG TCT GTT TCC ACA CCT GTC Lys Arg Lys Ser Val Ser Thr Pro Val 3240 TCT TGT AAA GGG GAG AAA GAG ATT GAT GAT Ser Cys Lys Gly Glu Lys Glu Ile Asp 3255 AGG ACA AGG ACT TGT GAT TTC TC ACA CCT GTC ACA ACT AGA ACT CCT GTC ACA CCT GTC Lys Gly Glu Lys Glu Ile Asp 3255 AGG ACA AGA GCC TTG GAT TTC TTC ACA ACT ACA ACT CCA CCT GTC ACA ACT ACA CCT GTC ACA CCT GTC ACA ACT ACA CCT GTC ACA ACT ACA AC	CTT TGC AAT GAA GCA GAA AAC AAC LEU CYS ASN GLU ALS ALEU MET 3180 GAT CCC AAG TGG TCC ACC CCA ACT LYS LEU MET 3190 ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC TTT GTT GTT GAT ACA ACA CCC ACC ACC ACC ACC ACC ACC A	CTT TGC AAT GGA GCA GAA AAC AAG CTT ATG CAT ASP PRO Lys Trp Ser Thr Pro Thr Lys Asp Cys 3190 ACT GCT CAA ATC ATC ATT CCT GGT ACA GGA AAC AAG Thr Ala Gln lle lle Tyr Tyr Gln Ser Pro Leu 3220 CCT AAT TGT GAG ATC ATT TCC ACA CCT GT GAT Ser Pro Leu 3225 AAA AGG AAG TCT GTT TCC ACA CTT TA AGA AGT CCT TTA Ser Cys Glu lle Tyr Tyr Gln Ser Pro Leu 3225 AAA AGG AAG TCT GTT GTT TCC ACA CTT GAT GAT GAC CAA Ser Cys Glu Leu Asp Phe Leu Ser Arg Leu Pro 3270 AGG AGA AGA GCC TTG GAT TCC TTG AGT AGA CTG CCT ATG AGA AGT CAA AGT CTG CTG ACA AGT AGT AGT AGT AGT AGT AGT AGT AGT AG	CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATG CAT AND ASD Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr 3190 ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT TAT ALA GLI	CUT TGC	CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT Leu Cys Ass Glu Ala Glu Ass Lys Leu Met His IIe Leu His 3185 GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGA ASP Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly 3199 ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT TCA ATA GAC GCT CAA ATC ATT CAT GIV Ass Cys Thr Ser Gly Asp Cys Thr Ala Gln Ile Ile Pro Gly Thr Gly Ass Lys Leu Leu Met 3205 CCT AAT TGT GAG ATA TAT TAT TAT CAA AGT CCT TTA TCA CTT TGT Pro Ass Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys 3220 AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr 3240 TCT TGT AAA GGG GAG AAA GAG AGT TGT AGT GAC CAA AAG ACT GC CAG ATG ACT Cys Arg Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Ass Cys 3265 AGA AGA GCC TTG GAT TTC TC ACA CAC CT GTC TCA GCC CAG ATG ACT Cys Arg	CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GAA AAC AAG CTC AAA GAC TCC AAA TTC CTG ATC ATG AAA AAA AAA AAA AAA AAA AAA AAA AAA	CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT LEU CYS ASS GLU ALS GLU ASS LYS LEU MET HIS ILL LEU HIS ALS ASS 3180 GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC ASS PRO LYS TRY SET THY PRO THY LYS ASS CYS THY SET GLY PRO TYY 3190 ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC CTT CTG ATG TCT TCT THY ALS GLU LEU MET SET SET SY 3205 ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAC CTT CTG ATG TCT TCT THY ALS GLU LEU MET SET SET SY 3205 CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TAT TCA CTT TGT ATG GCC PRO ASS CYS GLU ILE TYP TYP GLN SET PRO LEU SET LEU CYS MET ALS 2200 ACT GCT CAA ATC GTT GTT CC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG LYS ARG ACT CAT TGT AAA GGA CTC CAG ATG ACT TCA AAG LYS ARG ACT CAT AAA GGA CC CAG ATG ACT TCA AAG LYS ARG ACT CAT AAA GGA CTC CAG ATG ACT TCA AAG LYS ARG ACT CAG AAG AAC ACC CAG ATG ACT TCA AAG SET CYS LYS GLY GLU LYS GLU ILE ASS AAC AAC ACC CAG ATG ACT TCA AAG SET CYS LYS GLY GLU LYS GLU ILE ASS AAC ACC CAG ATG ACT CCA AAC ACC CTG TAT AAA GAC CTC TAT AAA AGA CC CAG ATG ACT TCA AAC ACC CAG ATG ACT CAC ACC CTG TAT AAA GAC CCC ACC TTG AAC ACC CAG ATG ACT CAC AAC ACC ACC CTG TAT AAC ACC CAC ACC ACC CTG TAT ACC ACC CTG GTT ACC ACC ACC ACC ACC ACC ACC ACC ACC A

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415

10485

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys 10 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe 25 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu 40 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr 55 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 70 75 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 85 90 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser 100 105 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 120 125 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 150 155 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr 165 170 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met 185 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val 190 200 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp 215 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu 230 235 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr 245 250 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn 260 265

Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala

Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met

Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly

Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala

Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys 1865 1870 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu 1940 1945 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser 1955 1960 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro

Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Pro Leu Asp Leu Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe

Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile

Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr Leu Arg Leu Lys Arg Cys Thr Thr Ser Leu Ile Lys Glu Glu Ger Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10485 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 229...10482
 - (D) OTHER INFORMATION: BRCA2 (OMI5)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AC.	AGAT'	FTGT	GAC	CGGC	GCG (1"1"1"(3T TT'	SCGG(CG G' CA G	TGGG' ሮሞሞል፣	TCGC	C GC	CGGG.	AGAA AAAG AA A? Me	GCG 'AAC 'IG C	CTGCGCC TGAGGGG TGCACCT CT ATT ro Ile	
GG/ Gl	A TC(/ Ser 5	C AAA	A GAC	3 AGG 1 Arg	G CCA J Pro	A ACA Thr	A TTT	r TT:	Γ GA e Gli	A ATT	T TT ≥ Pho 15	T AAG e Lys	7 7 67		C TGC G Cys	285
AAC Asr 20	C AAA 1 Lys	A GCA 8 Ala	A GAT Asp	TTA Leu	GGA Gly 25	A CCA	ATA	A AGT	r CTT	AAT Asr 30	TG(TTT Phe	GAA Glu	GAZ Glu	A CTT Leu 35	333
TCT Ser	TCA Ser	GAA Glu	GCT Ala	CCA Pro 40	. CCC Pro	TAT Tyr	' AAT Asn	TCT Ser	GAA Glu 45	CCT Pro	GCA Ala	A GAA a Glu	GAA Glu	TCT Ser 50	GAA Glu	381
CAT His	AAA Lys	AAC Asn	AAC Asn 55	AAT Asn	TAC Tyr	GAA Glu	CCA Pro	AAC Asn 60	CTA Leu	TTT Phe	' AAA Lys	ACT Thr	CCA Pro 65	CAA Gln	AGG Arg	429
AAA Lys	CCA Pro	TCT Ser 70	TAT Tyr	AAT Asn	CAG Gln	CTG Leu	GCT Ala 75	TCA Ser	ACT Thr	CCA Pro	ATA Ile	ATA Ile 80	TTC Phe	AAA Lys	GAG Glu	477
CAA Gln	GGG Gly 85	CTG Leu	ACT Thr	CTG Leu	CCG Pro	CTG Leu 90	TAC Tyr	CAA Gln	TCT Ser	CCT Pro	GTA Val 95	AAA Lys	GAA Glu	TTA Leu	GAT Asp	525
AAA Lys 100	TTC Phe	AAA Lys	TTA Leu	GAC Asp	TTA Leu 105	GGA Gly	AGG Arg	AAT Asn	GTT Val	CCC Pro 110	AAT Asn	AGT Ser	AGA Arg	CAT His	AAA Lys 115	573
AGT Ser	CTT Leu	CGC Arg	ACA Thr	GTG Val 120	AAA Lys	ACT Thr	AAA Lys	ATG Met	GAT Asp 125	CAA Gln	GCA Ala	GAT Asp	GAT Asp	GTT Val 130	TCC Ser	621
TGT Cys	CCA Pro	CTT Leu	CTA Leu 135	AAT Asn	TCT Ser	TGT Cys	CTT Leu	AGT Ser 140	GAA Glu	AGT Ser	CCT Pro	GTT Val	GTT Val 145	CTA Leu	CAA Gln	669
TGT	ACA	CAT	GTA	ACA	CCA	CAA	AGA	GAT	AAG	TCA	GTG	GTA	TGT	GGG	AGT	717

CAa	Thr	His 150	Val	Thr	Pro	Gln	Arg 155	Asp	Lys	Ser	Val	Val 160	Cys	Gly	Ser	
											CAG Gln 175					765
											GAT Asp					813
											ACT Thr					861
											CAT His					909
											AGT Ser					957
											AAC Asn 255					1005
											GGG Gly					1053
											ATG Met					1101
											TCT Ser			_		1149
											AAT Asn					1197
											GAA Glu 335					1245
											AAA Lys		_			1293
											GAT Asp					1341



1389

CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT

His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val

	375			380			385		
		TGT Cys							1437
		GAG Glu							1485
		GAA Glu 425							1533
		ACT Thr							1581
		 AAG Lys							1629
		CAT His							1677
		TCT Ser							1725
		ATA Ile 505							1773
		TCA Ser							1821
		GAA Glu							1869
		TTA Leu							1917
		CAG Gln							1965
		AAG Lys 585							2013
		AAA Lys							2061

			GCC Ala						2109
			GCT Ala	_					2157
			AAT Asn 650						2205
			ATT Ile						2253
			ATC Ile						2301
			CTA Leu						2349
			GAA Glu						2397
			AAA Lys 730						2445
			GTG Val						2493
			GAT Asp						2541
			GTT Val						2589
			ATG Met						2637
			ACC Thr 810						2685
			GAA Glu						2733

		AAA Lys														2781
		AAC Asn														2829
		ATT Ile 870														2877
		AAT Asn														2925
		GCT Ala														2973
		AAC Asn														3021
		GGT Gly														3069
		GTT Val 950														3117
		ACT Thr														3165
		ATA Ile														3213
		GGT Gly	Pro					Ser					Phe			3261
		AAT Asn					Leu					Ile				3309
	Met	TTC Phe L030				Ile					Pro					3357
Сув		GAA Glu			Asn					Asp						3405
AGC	AAG	CCT	CAG	TCA	ATT	AAT	ACT	GTA	TCT	GCA	CAT	TTA	CAG	AGT	AGT	3453

Ser 1060	Lys	Pro	Gln		Ile L065	Asn	Thr	Val		Ala 1070	His	Leu	Gln		Ser 1075	
			TCT Ser					Ser					Gln			3501
		Lys	CAG Gln 1095				Ser					Thr				3549
	Ala		ATT Ile			Leu					Glu					3597 ·
Gln			TTT Phe		Gln					Ser						3645
			GAA Glu	Val					Met					Thr		3693
			TGC Cys					Leu					Asn			3741
		Gly	CAG Gln 1175				Ser					Gly				3789
	Lys		AAG Lys			Gly					Asp					3837
Ala			TAT Tyr		Thr					Val						3885
			CAT His	Gly		Lys	Leu		Val	Ser	Thr			Leu		3933
			AAA Lys					I1e					Glu			3981
		Glu	GTA Val 1255				Ser					Lys				4029
	Val		TCA Ser			Lys					Asn					4077
			AAT Asn													4125

1285		1290	1	.295	
	Thr Gly Thr			GAA AAT TAC AA Glu Asn Tyr Ly	
				GCC AGT AGA AM Ala Ser Arg As 133	sn Ser
		Asp Gly Ser		AAA AAT GAT AG Lys Asn Asp Th 1345	
Cys Ile				ACT GAT CAG CAG Thr Asp Gln H: 1360	
			Phe Met Lys	GAG GGA AAC AG Glu Gly Asn Th .375	
	Glu Asp Leu			GAA GTT GCG AA Glu Val Ala Ly	
				GAA CAG TTA AG Glu Gln Leu Th 14:	nr Ala
		Asn Ile Lys		ACT TCT GAT AG Thr Ser Asp Tl 1425	
Phe Gln				GCC AAA GAG TO Ala Lys Glu So 1440	
			Gln Lys Pro	GAA GAA TTG CA Glu Glu Leu H: .455	
	Leu Asn Ser			AGA AAG AAC AA Arg Lys Asn Ly	
				AAA CAC AAA A Lys His Lys I 149	le Leu
		Val Gly Thr		CTA GTG ACC To Leu Val Thr Pl 1505	
Gly Gln				CCT ACT CTG T Pro Thr Leu Le 1520	

						AAG GAA TC Lys Glu Se	
				Glu Lys		GGT ACT AG Gly Thr Se	
	Ser Phe					AAG TAC AG Lys Tyr Ar 157	g Glu
						GAG ATC AC Glu Ile Th 1585	
Ala Pro 1				Asn Ser	Leu Asn A	AAT GAT AA Asn Asp Ly 500	
						rTA AGT GA' Seu Ser As	
				Lys Thr		AGT ATC TT Ser Ile Ph	
	Lys Val					GCA AAA AG Ala Lys Se: 165	r Pro
						ATT GAA AA' [le Glu As: 1665	
Ala Leu A				Ser Arg	Lys Thr S	CCT GTG AG Ser Val Se: 580	
		Glu Ala				GGA ATA TT Gly Ile Pho	
			Asn Thr	Ala Asp		GGA AAT TA' Gly Asn Ty:	
	7 7 CT 7 7 7 CT	ממ מטיד	AGT ACT	ATA GCT	GAA AAT O	BAC AAA AA'	r CAT 5421
	Asn Asn		Ser Thr	Ile Ala 1725	Glu Asn A	Asp Lys Asi 173	

	Tyr					Asp					GAT Asp					5517
Ser					Asp					Pro	GTA Val 1775					5565
				Asn					Lys		ATA Ile			Val		5613
			Ala					Val			GAT Asp		Cys			5661
		Val					Pro				AAA Lys	Asn				5709
	Leu					Ser					GTA Val					5757
Phe					${\tt Gly}$					Val	TCA Ser 1855					5805
				Asp					Ser		AGT Ser			Ile		5853
			Glu					Ile			ACG Thr		Ile			5901
		Tyr					Asp				ATT Ile	Leu				5949
	Asp					Ser					AAG Lys					5997
Ile					Ile					Gln	AAT Asn 1935					6045
				Lys					Asp		AGT Ser			Thr		6093
			Lys					Lys			AAG Lys		Val			6141
GCA	TAA	ACT	TGT	GGG	ATT	TTT	AGC	ACA	GCA	AGT	GGA	AAA	TCT	GTC	CAG	6189

Ala	Asn		Cys 1975	Gly	Ile	Phe		Thr 1980	Ala	Ser	Gly		Ser 1985	Val	Gln	
	TCA Ser					Gln					Val					6237
Glu	GAT Asp 2005				Gln					Val						6285
	CAT His			Gln					Glu					Arg		6333
	GAA Glu		Leu					Gly					Val			6381
	TCT Ser	Ala					Ser					Lys				6429
	TTA Leu					His					Val					6477
Asp	TTA Leu 2085				Glu					Tyr						6525
	AAT Asn			Lys					Val					Pro		6573
	TGT Cys		Asn					Lys					Glu			6621
	TCA Ser	Asn			Asn	Val	Glu		Gly			Glu				6669
	ATT Ile					Tyr					Gln					6717
Gln	TTG Leu 2165				Thr					Val						6765
	GGA Gly			Gln					Asn					Ile		6813
	ACT Thr															6861

2200	2205	2210

	Ser Lys Asp		TAC TTT GAA ACA Tyr Phe Glu Thr 2225	Glu Ala
	Lys Ala Phe		GAT GAA CTG ACA Asp Glu Leu The 2240	
AAA CTG CCA AGT Lys Leu Pro Ser 2245				
GAG GAA ATG GTT Glu Glu Met Val 2260		Ser Arg Ile		
Pro Leu Ile Leu			AAA AGA AAC TTA Lys Arg Asn Leu	
GAA TTT GAC AGG Glu Phe Asp Arg 2295				Ala Ser
AAA AGC ACT CCA Lys Ser Thr Pro 2310	Asp Gly Thr			
CAT GTT TCT TTA His Val Ser Leu 2325				
GAA CGT CAA GAG Glu Arg Gln Glu 2340		Pro Asn Phe		
TTT CTG TCT AAA Phe Leu Ser Lys				
TCA AGC AAT TTA Ser Ser Asn Leu 2375				Ser Ala
ACA AGA AAT GAA Thr Arg Asn Glu 2390	Lys Met Arg			
AAA GTC TTT GTT Lys Val Phe Val 2405				
GAA CAG TGT GTT Glu Gln Cys Val 2420		Asn Leu Glu		

AAC AT Asn Il		Gly					qaA					Ile			7581
AAT GA Asn Gl	u Ile					Lys					Gln				7629
GTA AC Val Th					Glu					Asp					7677
CTT CA Leu Gl 248	n Asn			Asp					Arg						7725
AGG CA Arg Gl			Phe					Ser					Lys		7773
TCC AC Ser Th		Pro					Lys					Gly			7821
CCC TC Pro Se	r Ala					Gln					Gly				7869
CAT TG His Cy					Ser					ser					7917
ACT GA Thr Gl 256	u Asp			Gly					${\tt Trp}$						7965
CAG TTG Gln Le 2580			Gly					Pro					Lys		8013
GGA AA Gly Ly		Glu					Leu					Gly			8061
CCA AA Pro Ly	s Leu					Trp					Tyr				8109
	s Leu : G AAA	Ile 2615 CTG	Ser GCA	Arg GCT	Ile ATG Met	Trp 2 GAA	Val 2620 TGT	Tyr GCC	Asn TTT	His CCT Pro	Tyr 2 AAG	Arg 2625 GAA	Trp	Ile GCT	81098157

		ACG Thr		Ile					Arg					Lys		8253
		AGG Arg	Asp					Lys					Cys			8301
		ATT Ile					Asn					Ser				8349
	Ser	AGT Ser 2710				Gln					Ile					8397
Gly		TAT Tyr			Lys					Pro						8445
		AAT Asn		Arg					Gln					His		8493
		CTG Leu	Val					Ala					Glu			8541
		CTT Leu 2					Ser					Arg				8589
	Tyr	ACC Thr 2790				Phe					Arg					8637
Pro		TCA Ser			Phe					Asn						8685
		ATT Ile		Arg					Gln					Thr		8733
		TTA Leu	Tyr					Glu					Lys			8781
		TAT Tyr					Gln					Ala				8829
	Ile	CAG Gln 2870				Glu					Asn					8877
TAT	TTA	CCA	TCA	CGT	GCA	CTA	ACA	AGA	CAG	CAA	GTT	CGT	GCT	TTG	CAA	8925

-	Leu 2885	Pro	Ser	Arg		Leu 2890	Thr	Arg	Gln		Val 2895	Arg	Ala	Leu	Gln	
				Leu				GTG Val	Lys					Pro		8973
			Gly					GAG Glu					Leu			9021
		Gln					Lys	AAA Lys 2940				Ile				9069
	Arg					Ser		GAA Glu			Glu					9117
Arg					Val			TTG Leu		Ile						9165
				Ser				AGT Ser	Ile					Ser		9213
			Leu					AAG Lys					Tyr			9261
		Ser					Lys	TCT Ser 3020				Asn				9309
	Ala					Gln		CAA Gln			Pro					9357
Ile			${\tt Gln}$	Ile	Tyr	Gln	Pro	CGG Arg	Glu	Pro	Leu	His				9405
				qaA				TCT Ser	Cys					Leu		9453
			Val					AAA Lys					Pro			9501
		Ser					Asn	TTA Leu 3100				Lys				9549
								CCT Pro								9597

3110 3115 3120

	Trp Arg Pro			CTT ACT TTA TTT Leu Thr Leu Phe	9645
				GAG GGC CAC TTT Glu Gly His Phe 3155	9693
		Met Lys Asn		AAT ATT GAC ATA Asn Ile Asp Ile 3170	9741
Leu Cys Asn				CTG CAT GCA AAT Leu His Ala Asn 3185	
			Asp Cys Thr	TCA GGG CCG TAC Ser Gly Pro Tyr 3200	
	Ile Ile Pro			CTG ATG TCT TCT Leu Met Ser Ser	
				CTT TGT ATG GCC Leu Cys Met Ala 3235	
		Thr Pro Val		ATG ACT TCA AAG Met Thr Ser Lys 3250	9981
Ser Cys Lys				AAC TGC AAA AAG Asn Cys Lys Lys 3265	10029
			Leu Pro Leu	CCT CCA CCT GTT Pro Pro Pro Val 3280	
	Cys Thr Phe			AAG GCA TTT CAG Lys Ala Phe Gln	
				ATA AAG AAA AAA Ile Lys Lys Lys 3315	10173
		Met Thr Pro		TTC AAT GAA ATT Phe Asn Glu Ile 3330	10221
Ser Leu Leu				CTT GCA TTG ATA Leu Ala Leu Ile 3345	10269

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3355 TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Glu Glu 3385 3390 AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 ATT ACA ACT AAA AAA TAT ATC TAA 10485 Ile Thr Thr Lys Lys Tyr Ile 3415

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe 25 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr 55 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 70 75 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 90 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 120 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 150 155 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr 170

Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met 180 185 Ser Trp Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val 200 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp 215 220 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu 230 235 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr 245 250 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn 265 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro 280 His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu 295 300 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu 310 315 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala 325 330 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr 345 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser 360 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser 375 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu 390 395 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile 410 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu 425 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg 440 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val 455 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys 470 475 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser 490 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro 505 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn 520 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr 535 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn 550 555 Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn 565 570 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr 585 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp 600 605 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala 615 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His

630 635 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr 645 650 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg 665 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr 680 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro 695 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp 710 715 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala 725 730 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp 745 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr 760 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly 795 790 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu 805 810 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu 825 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys 840 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln 855 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu 870 875 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn 885 890 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr 900 905 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val 92.0 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys 935 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys 950 955 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser 965 970 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys 985 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser 1000 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile 1015 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr 1030 1035 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln 1050 1045 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu 1065 Gln Ser Ser Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro 1075 1080

Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp 1270 1275 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Phe Glu Val Gly Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe

Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys

2435 2440 2445 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala Asn Arq Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asm Ala Ala

Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys

Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser

	3365 3370 3375	
	Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys 3380 3385 3390	
Glu	Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys 3395 3400 3405	
Gln	Asp Thr Ile Thr Thr Lys Lys Tyr Ile 3410 3415	
	(2) INFORMATION FOR SEQ ID NO:14:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE:	
	(A) NAME/KEY: other	
	(B) LOCATION: 120 (D) OTHER INFORMATION: 2F primer	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
	-	
TGAG	TTTTAC CTCAGTCACA	20
	(2) INFORMATION FOR SEQ ID NO:15:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
~~~	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
CAGG	BAAACAG CTATGACCCT GTGACGTACT GGGTTTTTAG C	41
	(2) INFORMATION FOR SEQ ID NO:16:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 3FII primer</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	

24

GATCTTTAAC TGTTCTGGGT CACA

<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE  (A) NAME/KEY: other  (B) LOCATION: 122  (D) OTHER INFORMATION: 3RII primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
CCCAGCATGA CACAATTAAT GA	22
(2) INFORMATION FOR SEQ ID NO:18:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 44 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 144 (D) OTHER INFORMATION: 4F/M 13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA	44
(2) INFORMATION FOR SEQ ID NO:19:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 4R-1A primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	

(2) INFORMATION FOR SEQ ID NO:17:

(2) INFORMATION FOR SEQ ID NO:20:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 140</li><li>(D) OTHER INFORMATION: 5+6F/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
TGTAAAACGA CGGCCAGTTG TGTTGGCATT TTAAACATCA	40
(2) INFORMATION FOR SEQ ID NO:21:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 138   (D) OTHER INFORMATION: 5+6R/M13R primer</pre>	*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT	38
(2) INFORMATION FOR SEQ ID NO:22:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other (B) LOCATION: 138	

ATCAGATTCA TCTTTATAGA AC

(D) OTHER INFORMATION: 7F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA	38
(2) INFORMATION FOR SEQ ID NO:23:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 36 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 136   (D) OTHER INFORMATION: 7R/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC	36
(2) INFORMATION FOR SEQ ID NO:24:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 140   (D) OTHER INFORMATION: 8F/M13F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
TGTAAAACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA	40
(2) INFORMATION FOR SEQ ID NO:25:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	

,一个人,我们是一个人,我们就是一个人,我们就是一个人,我们就是一个人,我们就是一个人,我们就是一个人,我们就是一个人,我们就是一个人,我们就是一个人,我们就是

(ix) FEATURE:

(A) NAME/KEY: other

(D) OTHER INFORMATION: 8FIA primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
TTGCATTCTA GTGATAATAT AC	22
(2) INFORMATION FOR SEQ ID NO:26:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 19 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 119</li><li>(D) OTHER INFORMATION: 8RIA primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
AATTGTTAGC AATTTCAAC	19
(2) INFORMATION FOR SEQ ID NO:27:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 140</li><li>(D) OTHER INFORMATION: 9F/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
TGTAAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT	40
(2) INFORMATION FOR SEQ ID NO:28:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	

(B) LOCATION: 1...22

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 140 (D) OTHER INFORMATION: 9R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA	40
(2) INFORMATION FOR SEQ ID NO:29:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 24 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 124</li><li>(D) OTHER INFORMATION: 10AF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GAATAATATA AATTATATGG CTTA	24
(2) INFORMATION FOR SEQ ID NO:30:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 37 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 137</li><li>(D) OTHER INFORMATION: 10AR/M13R primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT	37
(2) INFORMATION FOR SEQ ID NO:31:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 42 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: Other</li><li>(B) LOCATION: 142</li><li>(D) OTHER INFORMATION: 10BF/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
TGTAAAACGA CGGCCAGTAR CTGAAGTGGA ACCAAATGAT AC	42
(2) INFORMATION FOR SEQ ID NO:32:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 44 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 144</li><li>(D) OTHER INFORMATION: 10BR/M13R primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA	14
(2) INFORMATION FOR SEQ ID NO:33:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ix) FEATURE:	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 140</li><li>(D) OTHER INFORMATION: 10CF/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG	10
(2) INFORMATION FOR SEQ ID NO:34:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other</pre>	
(B) LOCATION: 119	
(D) OTHER INFORMATION: 10CRII primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
AGACAGAGGT ACCTGAATC	19
(2) INFORMATION FOR SEQ ID NO:35:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 40 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other (B) LOCATION: 140	
(D) OTHER INFORMATION: 11AF-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
TGTAAAACGA CGGCCAGTTG GTACTTTAAT TTTGTCACTT	40
(2) INFORMATION FOR SEQ ID NO:36:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 37 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other (B) LOCATION: 137	
(D) OTHER INFORMATION: 11AR-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT	37
(2) INFORMATION FOR SEQ ID NO:37:	

(B) TYPE: nucleic acid

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	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 122   (D) OTHER INFORMATION: 11BF primer</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
AAGAAG	ecaaa atgtaataag ga	22
	(2) INFORMATION FOR SEQ ID NO:38:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 122 (D) OTHER INFORMATION: 11BR primer	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
CATTTA	AAAGC ACATACATCT TG	22
	(2) INFORMATION FOR SEQ ID NO:39:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	<pre>(ix) FEATURE   (A) NAME/KEY: primer   (B) LOCATION:   (D) OTHER INFORMATION: 11CF primer</pre>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

(2) INFORMATION FOR SEQ ID NO:40:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>
(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11CR primer</li></ul>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
CAAGATTATT CCTTTCATTA GC 22
(2) INFORMATION FOR SEQ ID NO:41:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: Genomic DNA
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 122   (D) OTHER INFORMATION: 11DF primer</pre>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
AACCAAAACA CAAATCTAAG AG
(2) INFORMATION FOR SEQ ID NO:42:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 23 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>
(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE  (A) NAME/KEY: other  (B) LOCATION: 123  (D) OTHER INFORMATION: 11DR primer

TCTAGAGGCA AAGAATCATA C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
GTCATTTTA TATGCTGCTT TAC	23
(2) INFORMATION FOR SEQ ID NO:43:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	,
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other (B) LOCATION: 121 (D) OTHER INFORMATION: 11EF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
GGTTTTATAT GGAGACACAG G	21
(2) INFORMATION FOR SEQ ID NO:44:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 123   (D) OTHER INFORMATION: 11ER primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:</pre>	
GTATTTACAA TTTCAACACA AGC	23
(2) INFORMATION FOR SEQ ID NO:45:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	

(ix) FEATURE

(A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 11FF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
ATCACAGTTT TGGAGGTAGC	20
(2) INFORMATION FOR SEQ ID NO:46:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11FR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
CTGACTTCCT GATTCTTCTA A	21
(2) INFORMATION FOR SEQ ID NO:47:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11GF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
CTCAGATGTT ATTTTCCAAG C	21
(2) INFORMATION FOR SEQ ID NO:48:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(B) LOCATION: 121 (D) OTHER INFORMATION: 11GR primer
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
CTGTTAAATA ACCAGAAGCA C 21
(2) INFORMATION FOR SEQ ID NO:49:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 18 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: Genomic DNA
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 118</li><li>(D) OTHER INFORMATION: 11HF primer</li></ul>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
AGGTAGACAG CAGCAAGC
(2) INFORMATION FOR SEQ ID NO:50:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>
(ix) FEATURE:
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11HR primer</li></ul>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
GTAATATCAG TTGGCATTTA TT 22
(2) INFORMATION FOR SEQ ID NO:51:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>

(ix) FEATURE

<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 121</li><li>(D) OTHER INFORMATION: 11IF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
TGCAGAGGTA CATCCAATAA G	2 1
(2) INFORMATION FOR SEQ ID NO:52:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 121</li><li>(D) OTHER INFORMATION: 11IR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
GATCAGTAAA TAGCAAGTCC G	1
(2) INFORMATION FOR SEQ ID NO:53:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 23 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 123</li><li>(D) OTHER INFORMATION: 11JF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
TACTGAAAAT GAAGATAACA AAT	23
(2) INFORMATION FOR SEQ ID NO:54:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	

(2) INFORMATION FOR SEQ ID NO:55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: Genomic DNA  (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KF-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA  (2) INFORMATION FOR SEQ ID NO:56:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 122 (D) OTHER INFORMATION: 11JR primer	
(2) INFORMATION FOR SEQ ID NO:55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: Genomic DNA  (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KF-ML3 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA  (2) INFORMATION FOR SEQ ID NO:56:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: Genomic DNA  (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KF-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  TGTAAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA  (2) INFORMATION FOR SEQ ID NO:56:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	ATTTTGTTCT TTCTTATGTC AG	22
(A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: Genomic DNA  (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KF-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA  (2) INFORMATION FOR SEQ ID NO:56:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	(2) INFORMATION FOR SEQ ID NO:55:	
(ix) FEATURE  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KF-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA  (2) INFORMATION FOR SEQ ID NO:56:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	(A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KF-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA  (2) INFORMATION FOR SEQ ID NO:56:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	(ii) MOLECULE TYPE: Genomic DNA	
TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA  (2) INFORMATION FOR SEQ ID NO:56:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	(A) NAME/KEY: other (B) LOCATION: 135	
(2) INFORMATION FOR SEQ ID NO:56:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 35 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear   (A) NAME/KEY: other  (B) LOCATION: 135  (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 22 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA	3!
(A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (A) NAME/KEY: other (B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	(2) INFORMATION FOR SEQ ID NO:56:	
(B) LOCATION: 135 (D) OTHER INFORMATION: 11KR-M13 primer  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	<ul><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	
CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG  (2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 22 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	(B) LOCATION: 135	
(2) INFORMATION FOR SEQ ID NO:57:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 22 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG	3!
<ul><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	(2) INFORMATION FOR SEQ ID NO:57:	
	<ul><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	

<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 122   (D) OTHER INFORMATION: 11LF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	
CACAAAATAC TGAAAGAAAG TG	22
(2) INFORMATION FOR SEQ ID NO:58:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 19 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 119   (D) OTHER INFORMATION: 11LR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
GGCACCACAG TCTCAATAG	19
(2) INFORMATION FOR SEQ ID NO:59:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 11MF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
GCAAAGACCC TAAAGTACAG	20
(2) INFORMATION FOR SEQ ID NO:60:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11MR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
CATCAAATAT TCCTTCTCA AG	22
(2) INFORMATION FOR SEQ ID NO:61:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 135</li><li>(D) OTHER INFORMATION: 11NF-M13 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
TGTAAAACGA CGGCCAGTGA AAATTCAGCC TTAGC	35
(2) INFORMATION FOR SEQ ID NO:62:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 135</li><li>(D) OTHER INFORMATION: 11NR-M13 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT	35
(2) INFORMATION FOR SEQ ID NO:63:	

(A) LENGTH: 22 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(,	
(ix) FEATURE	
(A) NAME/KEY: other (B) LOCATION: 122	
(D) OTHER INFORMATION: 110F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
GTACTATAGC TGAAAATGAC AA 22	
(2) INFORMATION FOR SEQ ID NO:64:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 120	
(D) OTHER INFORMATION: 110R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
ACCACTGGCT ATCCTAAATG 20	
(2) INFORMATION FOR SEQ ID NO:65:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(C) STRANDEDNESS: SINGIE (D) TOPOLOGY: linear	
(0) 10101011 1111011	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 120 (D) OTHER INFORMATION: 11PF primer	
(D) OTHER INFORMATION. THE PITMET	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
TGAAGATATT TGCGTTGAGG 20	

(i) SEQUENCE CHARACTERISTICS:

	(2) INFORMATION FOR SEQ ID NO:66:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: Genomic DNA	
	<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 11PR primer</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
GTO	CAGCAAAA ACCTTATGTG	20
	(2) INFORMATION FOR SEQ ID NO:67:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11QF primer</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
ACC	GAAAATTA TGGCAGGTTG T	21
	(2) INFORMATION FOR SEQ ID NO:68:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 121</li><li>(D) OTHER INFORMATION: 11QR primer</li></ul>	

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
CTTGTCTTGC GTTTTGTAAT G	21
(2) INFORMATION FOR SEQ ID NO:69:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 11RF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
GCTTCATAAG TCAGTCTCAT	20
(2) INFORMATION FOR SEQ ID NO:70:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 11RR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
TCAAATTCCT CTAACACTCC	20
(2) INFORMATION FOR SEQ ID NO:71:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 35 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other	

(D) OTHER INFORMATION: 11SF-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC	3 5
(2) INFORMATION FOR SEQ ID NO:72:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 37 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 137</li><li>(D) OTHER INFORMATION: 11SR-M13 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT	37
(2) INFORMATION FOR SEQ ID NO:73:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11TF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
GTTCTTCAGA AAATAATCAC TC	22
(2) INFORMATION FOR SEQ ID NO:74:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(B) LOCATION: 1...35

(II) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11TR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
TGTAAAAAGA GAATGTGTGG C	21
(2) INFORMATION FOR SEQ ID NO:75:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 39 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 139</li><li>(D) OTHER INFORMATION: 11UF-M13 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
TGTAAAACGA CGGCCAGTAC TTTTTCTGAT GTTCCTGTG	3.9
(2) INFORMATION FOR SEQ ID NO:76:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 39 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other (B) LOCATION: 139 (D) OTHER INFORMATION: 11UR-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA	39
(2) INFORMATION FOR SEQ ID NO:77:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 42 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 142</li><li>(D) OTHER INFORMATION: 12F/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
TGTAAAACGA CGGCCAGTAG TGGTGTTTTA AAGTGGTCAA AA	42
(2) INFORMATION FOR SEQ ID NO:78:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 40 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 140</li><li>(D) OTHER INFORMATION: 12R/M13R primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
CAGGAAACAG CTATGACCGG ATCCACCTGA GGTCAGAATA	40
(2) INFORMATION FOR SEQ ID NO:79:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 13-2F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
TAACATTTAA GCATCCGTTA C	21

(2) INFORMATION FOR SEQ ID NO:80:

(A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 128   (D) OTHER INFORMATION: 13-2R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
AAACGAGACT TTTCTCATAC TGTATTAG	28
(2) INFORMATION FOR SEQ ID NO:81:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 14F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
ACCATGTAGC AAATGAGGGT CT	22
(2) INFORMATION FOR SEQ ID NO:82:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 122   (D) OTHER INFORMATION: 14AR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
GCTTTTGTCT GTTTTCCTCC AA	22

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:83:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 121</li><li>(D) OTHER INFORMATION: 15-2F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
CCAGGGGTTG TGCTTTTAA A	21
<ul> <li>(2) INFORMATION FOR SEQ ID NO:84:</li> <li>(i) SEQUENCE CHARACTERISTICS: <ul> <li>(A) LENGTH: 38 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: primer   (B) LOCATION:   (D) OTHER INFORMATION: 15FUT/M13-R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC	38
(2) INFORMATION FOR SEQ ID NO:85:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 24 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

- (ix) FEATURE
  - (A) NAME/KEY: other

  - (B) LOCATION: 1...24
    (D) OTHER INFORMATION: 16AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
TTTGGTTTGT TATAATTGTT TTTA	24
(2) INFORMATION FOR SEQ ID NO:86:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 16AR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
CCAACTTTT AGTTCGAGAG	20
(2) INFORMATION FOR SEQ ID NO:87:	
<ul><li>(i) 'SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 19 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 119   (D) OTHER INFORMATION: 17F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
TTCAGTATCA TCCTATGTG	19
(2) INFORMATION FOR SEQ ID NO:88:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other	

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:88:	
AGAAACCTTA	A ACCCATACTG	20
(	(2) INFORMATION FOR SEQ ID NO:89:	
( <i>P</i> (E	SEQUENCE CHARACTERISTICS: A) LENGTH: 39 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: single D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: Genomic DNA	
(	FEATURE (A) NAME/KEY: other (B) LOCATION: 139 (D) OTHER INFORMATION: 18FUT/M13-AF primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:89:	
TGTAAAACGA	A CGGCCAGTGA ATTCTAGAGT CACACTTCC	3 9
(	(2) INFORMATION FOR SEQ ID NO:90:	
A) E) (C	SEQUENCE CHARACTERISTICS: A) LENGTH: 38 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: single D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: Genomic DNA	
(	FEATURE (A) NAME/KEY: other (B) LOCATION: 138 (D) OTHER INFORMATION: 18R/M13R primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:90:	
CAGGAAACAG	CTATGACCTT TAACTGAATC AATGACTG	38
(	(2) INFORMATION FOR SEQ ID NO:91:	
(A (B (C	SEQUENCE CHARACTERISTICS:  A) LENGTH: 41 base pairs  B) TYPE: nucleic acid  C) STRANDEDNESS: single  D) TOPOLOGY: linear	

(B) LOCATION: 1...20

(D) OTHER INFORMATION: 17AR primer

(ii) MOLECULE TYPE: Genomic DNA

<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 141</li><li>(D) OTHER INFORMATION: 19F/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T	41
(2) INFORMATION FOR SEQ ID NO:92:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 39 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 139</li><li>(D) OTHER INFORMATION: 19FUT/M13-R primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
CAGGAAACAG CTATGACCAA GAGACCGAAA CTCCATCTC	39
(2) INFORMATION FOR SEQ ID NO:93:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 138</li><li>(D) OTHER INFORMATION: 20F/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
TGTAAAACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC	38
(2) INFORMATION FOR SEQ ID NO:94:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 39 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

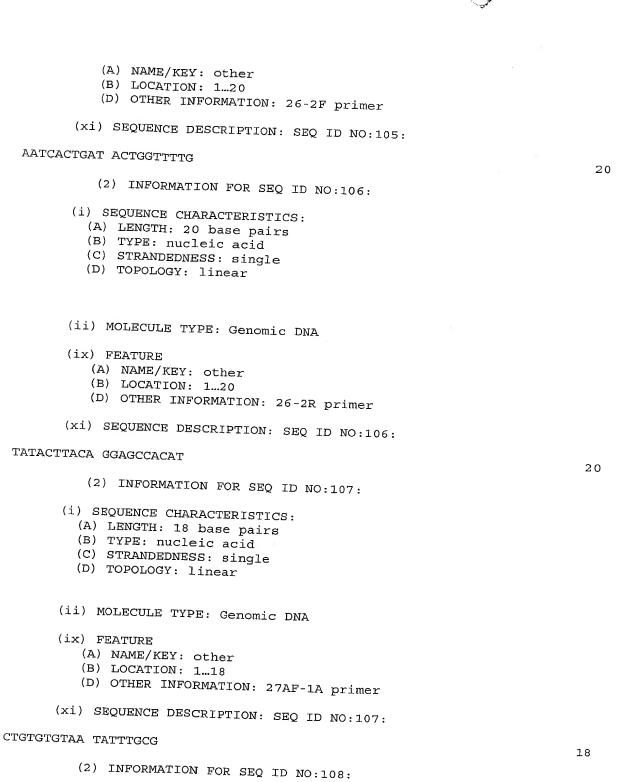
(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 139	
(D) OTHER INFORMATION: 20R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA	39
(2) INFORMATION FOR SEQ ID NO:95:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 39 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other</pre>	
(B) LOCATION: 139	
(D) OTHER INFORMATION: 21F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
TGTAAAACGA CGGCCAGTGG GTGTTTTATG CTTGGTTCT	39
(2) INFORMATION FOR SEQ ID NO:96:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 40 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other (B) LOCATION: 140	
(D) OTHER INFORMATION: 21R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:	
CAGGAAACAG CTATGACCCA TTTCAACATA TTCCTTCCTG	40
(2) INFORMATION FOR SEQ ID NO:97:	

<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 19 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 119</li><li>(D) OTHER INFORMATION: 22F-1A primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
AACCACACC TTAAGATGA	19
(2) INFORMATION FOR SEQ ID NO:98:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE  (A) NAME/KEY: other  (B) LOCATION: 120  (D) OTHER INFORMATION: 22R-1A primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:	
GCATTAGTAG TGGATTTTGC	20
(2) INFORMATION FOR SEQ ID NO:99:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 16 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 116</li><li>(D) OTHER INFORMATION: 23FII primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:	
TCACTTCCAT TGCATC	16

(2) INFORMATION FOR SEQ ID NO:100:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 17 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 117</li><li>(D) OTHER INFORMATION: 23RII primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
TGCCAACTGG TAGCTCC	17
(2) INFORMATION FOR SEQ ID NO:101:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE     (A) NAME/KEY: other     (B) LOCATION: 120     (D) OTHER INFORMATION: 24 2F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:	
TACAGTTAGC AGCGACAAAA	20
(2) INFORMATION FOR SEQ ID NO:102:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 138</li><li>(D) OTHER INFORMATION: 24R/M13R primer</li></ul>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:	
CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC	38
(2) INFORMATION FOR SEQ ID NO:103:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 25F-7/23 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	-
GCTTTCGCCA AATTCAGCTA	20
(2) INFORMATION FOR SEQ ID NO:104:	20
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 25R-7/23 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
TACCAAAATG TGTGGTGATG	20
(2) INFORMATION FOR SEQ ID NO:105:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(ix) FEATURE



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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE
(A) NAME/KEY: other (B) LOCATION: 140
(D) OTHER INFORMATION: 27AR/M13R primer
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:
CAGGAAACAG CTATGACGGC AAGTTCTTCG TCAGCTATTG
(2) INFORMATION FOR SEQ ID NO:109:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single (D) TOPOLOGY: linear
(b) Torobogi. Timear
(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE
(A) NAME/KEY: other
(B) LOCATION: 140
(D) OTHER INFORMATION: 27BF/M13F primer
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:
TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA
(2) INFORMATION FOR SEQ ID NO:110:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li></ul>
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE
(A) NAME/KEY: other (B) LOCATION: 138
(D) OTHER INFORMATION: 27BR/M13R primer
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA

40

38

(ii) MOLECULE TYPE: Genomic DNA